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(54) Title: NUCLEIC ACID FRAGMENTS AND POLYPEPTIDE FRAGMENTS DERIVED FROM <i>M. TUBERCULOSIS</i>		
(57) Abstract <p>The present invention is based on the identification and characterization of a number of <i>M. tuberculosis</i> derived novel proteins and protein fragments (SEQ ID NOS: 2, 4, 6, 8, 10, 12, 14, 16, 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, and 168-171). The invention is directed to the polypeptides and immunologically active fragments thereof, the genes encoding them, immunological compositions such as vaccines and skin test reagents containing the polypeptides. Another part of the invention is based on the surprising discovery that fusions between ESAT-6 and MPT59 are superior immunogens compared to each of the unfused proteins, respectively.</p>		

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NUCLEIC ACID FRAGMENTS AND POLYPEPTIDE FRAGMENTS DERIVED FROM M. TUBERCULOSIS

FIELD OF THE INVENTION

The present invention relates to a number of immunologically
5 active, novel polypeptide fragments derived from the *Mycobacterium tuberculosis*, vaccines and other immunologic compositions containing the fragments as immunogenic components, and methods of production and use of the polypeptides. The invention also relates to novel nucleic acid fragments derived
10 from *M. tuberculosis* which are useful in the preparation of the polypeptide fragments of the invention or in the diagnosis of infection with *M. tuberculosis*. The invention further relates to certain fusion polypeptides, notably fusions between ESAT-6 and MPT59.

15 BACKGROUND OF THE INVENTION

Human tuberculosis (hereinafter designated "TB") caused by *Mycobacterium tuberculosis* is a severe global health problem responsible for approximately 3 million deaths annually, according to the WHO. The worldwide incidence of new TB cases
20 has been progressively falling for the last decade but the recent years has markedly changed this trend due to the advent of AIDS and the appearance of multidrug resistant strains of *M. tuberculosis*.

The only vaccine presently available for clinical use is BCG,
25 a vaccine which efficacy remains a matter of controversy. BCG generally induces a high level of acquired resistance in animal models of TB, but several human trials in developing countries have failed to demonstrate significant protection. Notably, BCG is not approved by the FDA for use in the United
30 States.

This makes the development of a new and improved vaccine against TB an urgent matter which has been given a very high

priority by the WHO. Many attempts to define protective mycobacterial substances have been made, and from 1950 to 1970 several investigators reported an increased resistance after experimental vaccination. However, the demonstration of a specific long-term protective immune response with the potency of BCG has not yet been achieved by administration of soluble proteins or cell wall fragments, although progress is currently being made by relying on polypeptides derived from short term-culture filtrate, cf. the discussion below.

- 10 Immunity to *M. tuberculosis* is characterized by three basic features; i) Living bacilli efficiently induces a protective immune response in contrast to killed preparations; ii) Specifically sensitized T lymphocytes mediate this protection; iii) The most important mediator molecule seems to be
15 interferon gamma (INF- γ).

Short term-culture filtrate (ST-CF) is a complex mixture of proteins released from *M. tuberculosis* during the first few days of growth in a liquid medium (Andersen et al., 1991). Culture filtrates has been suggested to hold protective
20 antigens recognized by the host in the first phase of TB infection (Andersen et al. 1991, Orme et al. 1993). Recent data from several laboratories have demonstrated that experimental subunit vaccines based on culture filtrate antigens can provide high levels of acquired resistance to TB (Pal and
25 Horwitz, 1992; Roberts et al., 1995; Andersen, 1994; Lindblad et al., 1997). Culture filtrates are, however, complex protein mixtures and until now very limited information has been available on the molecules responsible for this protective immune response. In this regard, only two culture filtrate
30 antigens have been described as involved in protective immunity, the low mass antigen ESAT-6 (Andersen et al., 1995 and EP-A-0 706 571) and the 31 kDa molecule Ag85B (EP-0 432 203).

There is therefore a need for the identification of further antigens involved in the induction of protective immunity

against TB in order to eventually produce an effective sub-unit vaccine.

OBJECT OF THE INVENTION

It is an object of the invention to provide novel antigens
5 which are effective as components in a subunit vaccine against TB or which are useful as components in diagnostic compositions for the detection of infection with mycobacteria, especially virulence-associated mycobacteria. The novel antigens may also be important drug targets.

10 SUMMARY OF THE INVENTION

The present invention is i.a. based on the identification and characterization of a number of previously uncharacterized culture filtrate antigens from *M. tuberculosis*. In animal models of TB, T cells mediating immunity are focused predomi-
15 nantly to antigens in the regions 6-12 and 17-30 kDa of ST-CF. In the present invention 8 antigens in the low molecular weight region (CFP7, CFP7A, CFP7B, CFP8A, CFP8B, CFP9, CFP10A, and CFP11) and 18 antigens (CFP16, CFP17, CFP19, CFP19B, CFP20, CFP21, CFP22, CFP22A, CFP23, CFP23A, CFP23B,
20 CFP25, CFP26, CFP27, CFP28, CFP29, CFP30A, and CFP30B) in the 17-30 kDa region have been identified. Of these, CFP19A and CFP23 have been selected because they exhibit relatively high homologies with CFP21 and CFP25, respectively, in so far that a nucleotide homology sequence search in the Sanger Database
25 (cf. below) with the genes encoding CFP21 and CFP25, (cfp25 and cfp21 respectively), shows homology to two *M. tuberculosis* DNA sequences, orf19A and orf23. The two sequences, orf19a and orf23, encode to putative proteins CFP19A and CFP23 with the molecular weights of approx. 19 and 23 kDa
30 respectively. The identity, at amino acid level, to CFP21 and CFP25 is 46% and 50%, respectively, for both proteins. CFP21 and CFP25 have been shown to be dominant T-cell antigens, and it is therefore believed that CFP19A and CFP23 are possible new T-cell antigens.

Furthermore, a 50 kDa antigen (CFP50) has been isolated from culture filtrate and so has also an antigen (CWP32) isolated from the cell wall in the 30 kDa region.

5 The present invention is also based on the identification of a number of putative antigens from *M. tuberculosis* which are not present in *Mycobacterium bovis* BCG strains. The nucleotide sequences encoding these putative antigens are: *rd1-orf2*, *rd1-orf3*, *rd1-orf4*, *rd1-orf5*, *rd1-orf8*, *rd1-orf9a*, and *rd1-orf9b*.

10 Finally, the invention is based on the surprising discovery that fusions between ESAT-6 and MPT59 are superior immunogens compared to the unfused proteins, respectively.

The encoding genes for 33 of the antigens have been determined, the distribution of a number of the antigens in various mycobacterial strains investigated and the biological
15 activity of the products characterized. The panel hold antigens with potential for vaccine purposes as well as for diagnostic purposes, since the antigens are all secreted by metabolizing mycobacteria.

20 The following table lists the antigens of the invention by the names used herein as well as by reference to relevant SEQ ID NOs of N-terminal sequences, full amino acid sequences and sequences of DNA encoding the antigens:

	Antigen	N-terminal sequence SEQ ID NO:	Nucleotide sequence SEQ ID NO:	Amino acid sequence SEQ ID NO:
	CFP7		1	2
	CFP7A	81	47	48
	CFP7B	168	146	147
5	CFP8A	73	148	149
	CFP8B	74	150	151
	CFP9		3	4
	CFP10A	169	140	141
	CFP11	170	142	143
10	CFP16	79	63	64
	CFP17	17	5	6
	CFP19	82	49	50
	CFP19A		51	52
	CFP19B	80		
15	CFP20	18	7	8
	CFP21	19	9	10
	CFP22	20	11	12
	CFP22A	83	53	54
	CFP23		55	56
20	CFP23A	76		
	CFP23B	75		
	CFP25	21	13	14
	CFP25A	78	65	66
	CFP27	84	57	58
25	CFP28	22		
	CFP29	23	15	16
	CFP30A	85	59	60
	CFP30B	171	144	145
	CFP50	86	61	62
30	MPT51		41	42
	CWP32	77	152	153
	RD1-ORF8		67	68
	RD1-ORF2		71	72
	RD1-ORF9B		69	70
35	RD1-ORF3		87	88
	RD1-ORF9A		93	94
	RD1-ORF4		89	90
	RD1-ORF5		91	92
	MPT59-			172
40	ESAT6			
	ESAT6-			173
	MPT59			

It is well-known in the art that T-cell epitopes are responsible for the elicitation of the acquired immunity against TB, whereas B-cell epitopes are without any significant influence on acquired immunity and recognition of mycobacteria *in vivo*. Since such T-cell epitopes are linear and are known to have a minimum length of 6 amino acid residues, the

present invention is especially concerned with the identification and utilisation of such T-cell epitopes.

Hence, in its broadest aspect the invention relates to a substantially pure polypeptide fragment which

- 5 a) comprises an amino acid sequence selected from the sequences shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, and any one of 168-
10 171,
- b) comprises a subsequence of the polypeptide fragment defined in a) which has a length of at least 6 amino acid residues, said subsequence being immunologically equivalent to the polypeptide defined in a) with
15 respect to the ability of evoking a protective immune response against infections with mycobacteria belonging to the tuberculosis complex or with respect to the ability of eliciting a diagnostically significant
20 immune response indicating previous or ongoing sensitization with antigens derived from mycobacteria belonging to the tuberculosis complex, or
- c) comprises an amino acid sequence having a sequence identity with the polypeptide defined in a) or the subsequence defined in b) of at least 70% and at the
25 same time being immunologically equivalent to the polypeptide defined in a) with respect to the ability of evoking a protective immune response against infections with mycobacteria belonging to the tuberculosis complex or with respect to the ability of eliciting a
30 diagnostically significant immune response indicating previous or ongoing sensitization with antigens derived from mycobacteria belonging to the tuberculosis complex,

with the proviso that

- i) the polypeptide fragment is in essentially pure form when consisting of the amino acid sequence 1-96 of SEQ ID NO: 2 or when consisting of the amino acid sequence 87-108 of SEQ ID NO: 4 fused to β -galactosidase,
- ii) the degree of sequence identity in c) is at least 95% when the polypeptide comprises a homologue of a polypeptide which has the amino acid sequence SEQ ID NO: 12 or a subsequence thereof as defined in b), and
- iii) the polypeptide fragment contains a threonine residue corresponding to position 213 in SEQ ID NO: 42 when comprising an amino acid sequence of at least 6 amino acids in SEQ ID NO: 42.

Other parts of the invention pertains to the DNA fragments encoding a polypeptide with the above definition as well as to DNA fragments useful for determining the presence of DNA encoding such polypeptides.

DETAILED DISCLOSURE OF THE INVENTION

In the present specification and claims, the term "polypeptide fragment" denotes both short peptides with a length of at least two amino acid residues and at most 10 amino acid residues, oligopeptides (11-100 amino acid residues), and longer peptides (the usual interpretation of "polypeptide", i.e. more than 100 amino acid residues in length) as well as proteins (the functional entity comprising at least one peptide, oligopeptide, or polypeptide which may be chemically modified by being glycosylated, by being lipidated, or by comprising prosthetic groups). The definition of polypeptides also comprises native forms of peptides/proteins in mycobacteria as well as recombinant proteins or peptides in any type of expression vectors transforming any kind of host, and also chemically synthesized peptides.

In the present context the term "substantially pure polypeptide fragment" means a polypeptide preparation which contains at most 5% by weight of other polypeptide material with which it is natively associated (lower percentages of other polypeptide material are preferred, e.g. at most 4%, at most 3%, at most 2%, at most 1%, and at most $\frac{1}{2}\%$). It is preferred that the substantially pure polypeptide is at least 96% pure, i.e. that the polypeptide constitutes at least 96% by weight of total polypeptide material present in the preparation, and higher percentages are preferred, such as at least 97%, at least 98%, at least 99%, at least 99,25%, at least 99,5%, and at least 99,75%. It is especially preferred that the polypeptide fragment is in "essentially pure form", i.e. that the polypeptide fragment is essentially free of any other antigen with which it is natively associated, i.e. free of any other antigen from bacteria belonging to the tuberculosis complex. This can be accomplished by preparing the polypeptide fragment by means of recombinant methods in a non-mycobacterial host cell as will be described in detail below, or by synthesizing the polypeptide fragment by the well-known methods of solid or liquid phase peptide synthesis, e.g. by the method described by Merrifield or variations thereof.

The term "subsequence" when used in connection with a polypeptide of the invention having a SEQ ID NO selected from 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, and any one of 168-171 denotes any continuous stretch of at least 6 amino acid residues taken from the *M. tuberculosis* derived polypeptides in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171 and being immunological equivalent thereto with respect to the ability of conferring increased resistance to infections with bacteria belonging to the tuberculosis complex. Thus, included is also a

polypeptide from different sources, such as other bacteria or even from eukaryotic cells.

When referring to an "immunologically equivalent" polypeptide is herein meant that the polypeptide, when formulated in a vaccine or a diagnostic agent (*i.e.* together with a pharmaceutically acceptable carrier or vehicle and optionally an adjuvant), will

- I) confer, upon administration (either alone or as an immunologically active constituent together with other antigens), an acquired increased specific resistance in a mouse and/or in a guinea pig and/or in a primate such as a human being against infections with bacteria belonging to the tuberculosis complex which is at least 20% of the acquired increased resistance conferred by *Mycobacterium bovis* BCG and also at least 20% of the acquired increased resistance conferred by the parent polypeptide comprising SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171 (said parent polypeptide having substantially the same relative location and pattern in a 2DE gel prepared as the 2DE gel shown in Fig. 6, cf. the examples), the acquired increased resistance being assessed by the observed reduction in mycobacterial counts from spleen, lung or other organ homogenates isolated from the mouse or guinea pig receiving a challenge infection with a virulent strain of *M. tuberculosis*, or, in a primate such as a human being, being assessed by determining the protection against development of clinical tuberculosis in a vaccinated group versus that observed in a control group receiving a placebo or BCG (preferably the increased resistance is higher and corresponds to at least 50% of the protective immune response elicited by *M. bovis* BCG, such as at least 60%, or even more preferred to at least 80% of

the protective immune response elicited by *M. bovis* BCG, such as at least 90%; in some cases it is expected that the increased resistance will supersede that conferred by *M. bovis* BCG, and hence it is preferred that the resistance will be at least 100%, such as at least 110% of said increased resistance); and/or

- II) elicit a diagnostically significant immune response in a mammal indicating previous or ongoing sensitization with antigens derived from mycobacteria belonging to the tuberculosis complex; this diagnostically significant immune response can be in the form of a delayed type hypersensitivity reaction which can e.g. be determined by a skin test, or can be in the form of IFN- γ release determined e.g. by an IFN- γ assay/as described in detail below. A diagnostically significant response in a skin test setup will be a reaction which gives rise to a skin reaction which is at least 5 mm in diameter and which is at least 65% (preferably at least 75% such as at the least 85%) of the skin reaction (assessed as the skin reaction diameter) elicited by the parent polypeptide comprising SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171.

The ability of the polypeptide fragment to confer increased immunity may thus be assessed by measuring in an experimental animal, e.g. a mouse or a guinea pig, the reduction in mycobacterial counts from the spleen, lung or other organ homogenates isolated from the experimental animal which have received a challenge infection with a virulent strain of mycobacteria belonging to the tuberculosis complex after previously having been immunized with the polypeptide, as compared to the mycobacterial counts in a control group of experimental animals infected with the same virulent strain, which experimental animals have not previously been immunized

against tuberculosis. The comparison of the mycobacterial counts may also be carried out with mycobacterial counts from a group of experimental animals receiving a challenge infection with the same virulent strain after having been immunized with *Mycobacterium bovis* BCG.

The mycobacterial counts in homogenates from the experimental animals immunized with a polypeptide fragment according to the present invention must at the most be 5 times the counts in the mice or guinea pigs immunized with *Mycobacterium bovis* BCG, such as at the most 3 times the counts, and preferably at the most 2 times the counts.

A more relevant assessment of the ability of the polypeptide fragment of the invention to confer increased resistance is to compare the incidence of clinical tuberculosis in two groups of individuals (e.g. humans or other primates) where one group receives a vaccine as described herein which contains an antigen of the invention and the other group receives either a placebo or an other known TB vaccine (e.g. BCG). In such a setup, the antigen of the invention should give rise to a protective immunity which is significantly higher than the one provided by the administration of the placebo (as determined by statistical methods known to the skilled artisan).

The "tuberculosis-complex" has its usual meaning, i.e. the complex of mycobacteria causing TB which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium bovis* BCG, and *Mycobacterium africanum*.

In the present context the term "metabolizing mycobacteria" means live mycobacteria that are multiplying logarithmically and releasing polypeptides into the culture medium wherein they are cultured.

The term "sequence identity" indicates a quantitative measure of the degree of homology between two amino acid sequences or

between two nucleotide sequences of equal length: The sequence identity can be calculated as $\frac{(N_{ref}-N_{dif})100}{N_{ref}}$, wherein

N_{dif} is the total number of non-identical residues in the two sequences when aligned and wherein N_{ref} is the number of
5 residues in one of the sequences. Hence, the DNA sequence AGTCAGTC will have a sequence identity of 75% with the sequence AATCAATC ($N_{dif}=2$ and $N_{ref}=8$).

The sequence identity is used here to illustrate the degree of identity between the amino acid sequence of a given
10 polypeptide and the amino acid sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171. The amino acid sequence to be compared with the amino
15 acid sequence shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171 may be deduced from a DNA sequence, e.g. obtained by hybridization as defined
20 below, or may be obtained by conventional amino acid sequencing methods. The sequence identity is preferably determined on the amino acid sequence of a mature polypeptide, i.e. without taking any leader sequence into consideration.

As appears from the above disclosure, polypeptides which are
25 not identical to the polypeptides having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171 are embraced by the present invention. The invention allows for
30 minor variations which do not have an adverse effect on immunogenicity compared to the parent sequences and which may give interesting and useful novel binding properties or biological functions and immunogenicities etc.

Each polypeptide fragment may thus be characterized by specific amino acid and nucleic acid sequences. It will be understood that such sequences include analogues and variants produced by recombinant methods wherein such nucleic acid and polypeptide sequences have been modified by substitution, insertion, addition and/or deletion of one or more nucleotides in said nucleic acid sequences to cause the substitution, insertion, addition or deletion of one or more amino acid residues in the recombinant polypeptide. When the term DNA is used in the following, it should be understood that for the number of purposes where DNA can be substituted with RNA, the term DNA should be read to include RNA embodiments which will be apparent for the man skilled in the art. For the purposes of hybridization, PNA may be used instead of DNA, as PNA has been shown to exhibit a very dynamic hybridization profile (PNA is described in Nielsen P E et al., 1991, Science 254: 1497-1500).

In both immunodiagnostics and vaccine preparation, it is often possible and practical to prepare antigens from segments of a known immunogenic protein or polypeptide. Certain epitopic regions may be used to produce responses similar to those produced by the entire antigenic polypeptide. Potential antigenic or immunogenic regions may be identified by any of a number of approaches, e.g., Jameson-Wolf or Kyte-Doolittle antigenicity analyses or Hopp and Woods (1981) hydrophobicity analysis (see, e.g., Jameson and Wolf, 1988; Kyte and Doolittle, 1982; or U.S. Patent No. 4,554,101). Hydrophobicity analysis assigns average hydrophilicity values to each amino acid residue from these values average hydrophilicities can be calculated and regions of greatest hydrophilicity determined. Using one or more of these methods, regions of predicted antigenicity may be derived from the amino acid sequence assigned to the polypeptides of the invention.

Alternatively, in order to identify relevant T-cell epitopes which are recognized during an immune response, it is also possible to use a "brute force" method: Since T-cell epitopes

are linear, deletion mutants of polypeptides having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171 will, if constructed systematically, reveal what regions of the polypeptides are essential in immune recognition, e.g. by subjecting these deletion mutants to the IFN- γ assay described herein. Another method utilises overlapping oligomers (preferably synthetic having a length of e.g. 20 amino acid residues) derived from polypeptides having SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171. Some of these will give a positive response in the IFN- γ assay whereas others will not.

In a preferred embodiment of the invention, the polypeptide fragment of the invention comprises an epitope for a T-helper cell.

Although the minimum length of a T-cell epitope has been shown to be at least 6 amino acids, it is normal that such epitopes are constituted of longer stretches of amino acids. Hence it is preferred that the polypeptide fragment of the invention has a length of at least 7 amino acid residues, such as at least 8, at least 9, at least 10, at least 12, at least 14, at least 16, at least 18, at least 20, at least 22, at least 24, and at least 30 amino acid residues.

As will appear from the examples, a number of the polypeptides of the invention are natively translation products which include a leader sequence (or other short peptide sequences), whereas the product which can be isolated from short-term culture filtrates from bacteria belonging to the tuberculosis complex are free of these sequences. Although it may in some applications be advantageous to produce these polypeptides recombinantly and in this connection facilitate export of the polypeptides from the host cell by including

information encoding the leader sequence in the gene for the polypeptide, it is more often preferred to either substitute the leader sequence with one which has been shown to be superior in the host system for effecting export, or to
5 totally omit the leader sequence (e.g. when producing the polypeptide by peptide synthesis. Hence, a preferred embodiment of the invention is a polypeptide which is free from amino acid residues -30 to -1 in SEQ ID NO: 6 and/or -32 to -1 in SEQ ID NO: 10 and/or -8 to -1 in SEQ ID NO: 12 and/or
10 -32 to -1 in SEQ ID NO: 14 and/or -33 to -1 in SEQ ID NO: 42 and/or -38 to -1 in SEQ ID NO: 52 and/or -33 to -1 in SEQ ID NO: 56 and/or -56 to -1 in SEQ ID NO: 58 and/or -28 to -1 in SEQ ID NO: 151.

In another preferred embodiment, the polypeptide fragment of
15 the invention is free from any signal sequence; this is especially interesting when the polypeptide fragment is produced synthetically but even when the polypeptide fragments are produced recombinantly it is normally acceptable that they are not exported by the host cell to the periplasm
20 or the extracellular space; the polypeptide fragments can be recovered by traditional methods (cf. the discussion below) from the cytoplasm after disruption of the host cells, and if there is need for refolding of the polypeptide fragments, general refolding schemes can be employed, cf. e.g. the
25 disclosure in WO 94/18227 where such a general applicable refolding method is described.

A suitable assay for the potential utility of a given polypeptide fragment derived from SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60,
30 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, or any one of 168-171 is to assess the ability of the polypeptide fragment to effect IFN- γ release from primed memory T-lymphocytes. Polypeptide fragments which have this capability are according to the
35 invention especially interesting embodiments of the invention: It is contemplated that polypeptide fragments which

stimulate T lymphocyte immune response shortly after the onset of the infection are important in the control of the mycobacteria causing the infection before the mycobacteria have succeeded in multiplying up to the number of bacteria
5 that would have resulted in fulminant infection.

Thus, an important embodiment of the invention is a polypeptide fragment defined above which

- 1) induces a release of IFN- γ from primed memory T-lymphocytes withdrawn from a mouse within 2 weeks of primary
10 infection or within 4 days after the mouse has been re-challenge infected with mycobacteria belonging to the tuberculosis complex, the induction performed by the addition of the polypeptide to a suspension comprising about 200,000 spleen cells per ml, the addition of the
15 polypeptide resulting in a concentration of 1-4 μ g polypeptide per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 2 days after the addition of the polypeptide to the suspension, and/or
- 20 2) induces a release of IFN- γ of at least 1,500 pg/ml above background level from about 1,000,000 human PBMC (peripheral blood mononuclear cells) per ml isolated from TB patients in the first phase of infection, or from healthy BCG vaccinated donors, or from healthy
25 contacts to TB patients, the induction being performed by the addition of the polypeptide to a suspension comprising the about 1,000,000 PBMC per ml, the addition of the polypeptide resulting in a concentration of 1-4 μ g polypeptide per ml suspension, the release of
30 IFN- γ being assessable by determination of IFN- γ in supernatant harvested 2 days after the addition of the polypeptide to the suspension; and/or
- 3) induces an IFN- γ release from bovine PBMC derived from animals previously sensitized with mycobacteria belong-

ing to the tuberculosis complex, said release being at least two times the release observed from bovine PBMC derived from animals not previously sensitized with mycobacteria belonging to the tuberculosis complex.

- 5 Preferably, in alternatives 1 and 2, the release effected by the polypeptide fragment gives rise to at least 1,500 pg/ml IFN- γ in the supernatant but higher concentrations are preferred, e.g. at least 2,000 pg/ml and even at least 3,000 pg/ml IFN- γ in the supernatant. The IFN- γ release from bovine
10 PBMC can e.g. be measured as the optical density (OD) index over background in a standard cytokine ELISA and should thus be at least two, but higher numbers such as at least 3, 5, 8, and 10 are preferred.

- The polypeptide fragments of the invention preferably comprises an amino acid sequence of at least 6 amino acid residues in length which has a higher sequence identity than 70 percent with SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, any one of 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, any one of 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149,
20 151, 153, or any one of 168-171. A preferred minimum percentage of sequence identity is at least 80%, such as at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, and at least 99.5%.

- 25 As mentioned above, it will normally be interesting to omit the leader sequences from the polypeptide fragments of the invention. However, by producing fusion polypeptides, superior characteristics of the polypeptide fragments of the invention can be achieved. For instance, fusion partners
30 which facilitate export of the polypeptide when produced recombinantly, fusion partners which facilitate purification of the polypeptide, and fusion partners which enhance the immunogenicity of the polypeptide fragment of the invention are all interesting possibilities. Therefore, the invention
35 also pertains to a fusion polypeptide comprising at least one

polypeptides such as INF- γ , IL-2 and IL-12. In order to facilitate expression and/or purification
15 the fusion partner can e.g. be a bacterial fimbrial protein, e.g. the pilus components pilin and papA; protein A; the ZZ-peptide (ZZ-fusions are marketed by Pharmacia in Sweden); the maltose binding protein; glutathione S-transferase; β -galactosidase; or poly-histidine.

20 Other interesting fusion partners are polypeptides which are lipidated and thereby effect that the immunogenic polypeptide is presented in a suitable manner to the immune system. This effect is e.g. known from vaccines based on the *Borrelia burgdorferi* OspA polypeptide, wherein the lipidated membrane
25 anchor in the polypeptide confers a self-adjuvating effect to the polypeptide (which is natively lipidated) when isolated from cells producing it. In contrast, the OspA polypeptide is relatively silent immunologically when prepared without the lipidation anchor.

30 As evidenced in Example 6A, the fusion polypeptide consisting of MPT59 fused directly N-terminally to ESAT-6 enhances the immunogenicity of ESAT-6 beyond what would be expected from the immunogenicities of MPT59 and ESAT-6 alone. The precise
35 reason for this surprising finding is not yet known, but it is expected that either the presence of both antigens lead to a synergistic effect with respect to immunogenicity or the

presence of a sequence N-terminally to the ESAT-6 sequence protects this immune dominant protein from loss of important epitopes known to be present in the N-terminus. A third, alternative, possibility is that the presence of a sequence C-terminally to the MPT59 sequence enhances the immunologic properties of this antigen.

Hence, one part of the invention pertains to a fusion polypeptide fragment which comprises a first amino acid sequence including at least one stretch of amino acids constituting a T-cell epitope derived from the *M. tuberculosis* protein ESAT-6 or MPT59, and a second amino acid sequence including at least one T-cell epitope derived from a *M. tuberculosis* protein different from ESAT-6 (if the first stretch of amino acids are derived from ESAT-6) or MPT59 (if the first stretch of amino acids are derived from MPT59) and/or including a stretch of amino acids which protects the first amino acid sequence from *in vivo* degradation or post-translational processing. The first amino acid sequence may be situated N- or C-terminally to the second amino acid sequence, but in line with the above considerations regarding protection of the ESAT-6 N-terminus it is preferred that the first amino acid sequence is C-terminal to the second when the first amino acid sequence is derived from ESAT-6.

Although only the effect of fusion between MPT59 and ESAT6 has been investigated at present, it is believed that ESAT6 and MPT59 or epitopes derived therefrom could be advantageously be fused to other fusion partners having substantially the same effect on overall immunogenicity of the fusion construct. Hence, it is preferred that such a fusion polypeptide fragment according of the invention is one, wherein the at least one T-cell epitope included in the second amino acid sequence is derived from a *M. tuberculosis* polypeptide (the "parent" polypeptide) selected from the group consisting of a polypeptide fragment according to the present invention and described in detail above and in the examples, or the amino acid sequence could be derived from

any one of the *M. tuberculosis* proteins DnaK, GroEL, urease, glutamine synthetase, the proline rich complex, L-alanine dehydrogenase, phosphate binding protein, Ag 85 complex, HBHA (heparin binding hemagglutinin), MPT51, MPT64, superoxide
5 dismutase, 19 kDa lipoprotein, α -crystallin, GroES, MPT59 (when the first amino acid sequence is derived from ESAT-6), and ESAT-6 (when the first amino acid sequence is derived from MPT59). It is preferred that the first and second T-cell
10 epitopes each have a sequence identity of at least 70% with the natively occurring sequence in the proteins from which they are derived and it is even further preferred that the first and/or second amino acid sequence has a sequence identity of at least 70% with the protein from which they are
15 derived. A most preferred embodiment of this fusion polypeptide is one wherein the first amino acid sequence is the amino acid sequence of ESAT-6 or MPT59 and/or the second amino acid sequence is the full-length amino acid sequence of the possible "parent" polypeptides listed above.

In the most preferred embodiment, the fusion polypeptide
20 fragment comprises ESAT-6 fused to MPT59 (advantageously, ESAT-6 is fused to the C-terminus of MPT59) and in one special embodiment, there are no linkers introduced between the two amino acid sequences constituting the two parent polypeptide fragments.

25 Another part of the invention pertains to a nucleic acid fragment in isolated form which

- 1) comprises a nucleic acid sequence which encodes a polypeptide or fusion polypeptide as defined above, or
30 comprises a nucleic acid sequence complementary thereto, and/or
- 2) has a length of at least 10 nucleotides and hybridizes readily under stringent hybridization conditions (as defined in the art, i.e. 5-10°C under the melting point T_m , cf. Sambrook et al, 1989, pages 11.45-11.49) with a

nucleic acid fragment which has a nucleotide sequence selected from

5 SEQ ID NO: 1 or a sequence complementary thereto,
SEQ ID NO: 3 or a sequence complementary thereto,
SEQ ID NO: 5 or a sequence complementary thereto,
SEQ ID NO: 7 or a sequence complementary thereto,
SEQ ID NO: 9 or a sequence complementary thereto,
SEQ ID NO: 11 or a sequence complementary thereto,
SEQ ID NO: 13 or a sequence complementary thereto,
10 SEQ ID NO: 15 or a sequence complementary thereto,
SEQ ID NO: 41 or a sequence complementary thereto,
SEQ ID NO: 47 or a sequence complementary thereto,
SEQ ID NO: 49 or a sequence complementary thereto,
SEQ ID NO: 51 or a sequence complementary thereto,
15 SEQ ID NO: 53 or a sequence complementary thereto,
SEQ ID NO: 55 or a sequence complementary thereto,
SEQ ID NO: 57 or a sequence complementary thereto,
SEQ ID NO: 59 or a sequence complementary thereto,
SEQ ID NO: 61 or a sequence complementary thereto,
20 SEQ ID NO: 63 or a sequence complementary thereto,
SEQ ID NO: 65 or a sequence complementary thereto,
SEQ ID NO: 67 or a sequence complementary thereto,
SEQ ID NO: 69 or a sequence complementary thereto,
SEQ ID NO: 71 or a sequence complementary thereto,
25 SEQ ID NO: 87 or a sequence complementary thereto,
SEQ ID NO: 89 or a sequence complementary thereto,
SEQ ID NO: 91 or a sequence complementary thereto,
SEQ ID NO: 93 or a sequence complementary thereto,
SEQ ID NO: 140 or a sequence complementary thereto,
30 SEQ ID NO: 142 or a sequence complementary thereto,
SEQ ID NO: 144 or a sequence complementary thereto,
SEQ ID NO: 146 or a sequence complementary thereto,
SEQ ID NO: 148 or a sequence complementary thereto,
SEQ ID NO: 150 or a sequence complementary thereto, and
35 SEQ ID NO: 152 or a sequence complementary thereto,

with the proviso that when the nucleic acid fragment comprises a subsequence of SEQ ID NO: 41, then the nucleic acid

fragment contains an A corresponding to position 781 in SEQ ID NO: 41 and when the nucleic acid fragment comprises a subsequence of a nucleotide sequence exactly complementary to SEQ ID NO: 41, then the nucleic acid fragment comprises a T
5 corresponding to position 781 in SEQ ID NO: 41.

It is preferred that the nucleic acid fragment is a DNA fragment.

To provide certainty of the advantages in accordance with the invention, the preferred nucleic acid sequence when employed
10 for hybridization studies or assays includes sequences that are complementary to at least a 10 to 40, or so, nucleotide stretch of the selected sequence. A size of at least 10 nucleotides in length helps to ensure that the fragment will be of sufficient length to form a duplex molecule that is
15 both stable and selective. Molecules having complementary sequences over stretches greater than 10 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules obtained.

20 Hence, the term "subsequence" when used in connection with the nucleic acid fragments of the invention is intended to indicate a continuous stretch of at least 10 nucleotides exhibits the above hybridization pattern. Normally this will require a minimum sequence identity of at least 70% with a
25 subsequence of the hybridization partner having SEQ ID NO: 1, 3, 5, 7, 9, 11, 12, 15, 21, 41, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 87, 89, 91, 93, 140, 142, 144, 146, 148, 150, or 152. It is preferred that the nucleic acid fragment is longer than 10 nucleotides, such as at least 15,
30 at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, and at least 80 nucleotides long, and the sequence identity should preferable also be higher than 70%, such as at least 75%, at least 80%, at least 85%, at
35 least 90%, at least 92%, at least 94%, at least 96%, and at

least 98%. It is most preferred that the sequence identity is 100%. Such fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, by application of nucleic acid reproduction technology, such as the PCR technology of U.S. Patent 4,603,102, or by introducing selected sequences into recombinant vectors for recombinant production.

It is well known that the same amino acid may be encoded by various codons, the codon usage being related, *inter alia*, to the preference of the organisms in question expressing the nucleotide sequence. Thus, at least one nucleotide or codon of a nucleic acid fragment of the invention may be exchanged by others which, when expressed, result in a polypeptide identical or substantially identical to the polypeptide encoded by the nucleic acid fragment in question. The invention thus allows for variations in the sequence such as substitution, insertion (including introns), addition, deletion and rearrangement of one or more nucleotides, which variations do not have any substantial effect on the polypeptide encoded by the nucleic acid fragment or a subsequence thereof. The term "substitution" is intended to mean the replacement of one or more nucleotides in the full nucleotide sequence with one or more different nucleotides, "addition" is understood to mean the addition of one or more nucleotides at either end of the full nucleotide sequence, "insertion" is intended to mean the introduction of one or more nucleotides within the full nucleotide sequence, "deletion" is intended to indicate that one or more nucleotides have been deleted from the full nucleotide sequence whether at either end of the sequence or at any suitable point within it, and "rearrangement" is intended to mean that two or more nucleotide residues have been exchanged with each other.

The nucleotide sequence to be modified may be of cDNA or genomic origin as discussed above, but may also be of synthetic origin. Furthermore, the sequence may be of mixed cDNA and genomic, mixed cDNA and synthetic or genomic and syn-

thetic origin as discussed above. The sequence may have been modified, e.g. by site-directed mutagenesis, to result in the desired nucleic acid fragment encoding the desired polypeptide. The following discussion focused on modifications of nucleic acid encoding the polypeptide should be understood to encompass also such possibilities, as well as the possibility of building up the nucleic acid by ligation of two or more DNA fragments to obtain the desired nucleic acid fragment, and combinations of the above-mentioned principles.

The nucleotide sequence may be modified using any suitable technique which results in the production of a nucleic acid fragment encoding a polypeptide of the invention.

The modification of the nucleotide sequence encoding the amino acid sequence of the polypeptide of the invention should be one which does not impair the immunological function of the resulting polypeptide.

A preferred method of preparing variants of the antigens disclosed herein is site-directed mutagenesis. This technique is useful in the preparation of individual peptides, or biologically functional equivalent proteins or peptides, derived from the antigen sequences, through specific mutagenesis of the underlying nucleic acid. The technique further provides a ready ability to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the nucleic acid. Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the nucleotide sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Typically, a primer of about 17 to 25 nucle-

otides in length is preferred, with about 5 to 10 residues on both sides of the junction of the sequence being altered.

In general, the technique of site-specific mutagenesis is well known in the art as exemplified by publications (Adelman
5 et al., 1983). As will be appreciated, the technique typically employs a phage vector which exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage (Messing et al., 1981). These phage are readily commercially
10 available and their use is generally well known to those skilled in the art.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector which includes within its sequence a nucleic acid sequence
15 which encodes the polypeptides of the invention. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically, for example by the method of Crea et al. (1978). This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing
20 enzymes such as E. coli polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector
25 is then used to transform appropriate cells, such as E. coli cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected nucleic acid fragments of the invention using site-directed mutagenesis is provided as a means of producing potentially useful
30 species of the genes and is not meant to be limiting as there are other ways in which sequence variants of the nucleic acid fragments of the invention may be obtained. For example, recombinant vectors encoding the desired genes may be treated
35 with mutagenic agents to obtain sequence variants (see, e.g.,

a method described by Eichenlaub, 1979) for the mutagenesis of plasmid DNA using hydroxylamine.

The invention also relates to a replicable expression vector which comprises a nucleic acid fragment defined above, especially a vector which comprises a nucleic acid fragment
5 encoding a polypeptide fragment of the invention.

The vector may be any vector which may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to
10 be introduced. Thus, the vector may be an autonomously replicating vector, i.e. a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication; examples of such a vector are a plasmid, phage, cosmid, mini-chromosome or virus. Alterna-
15 tively, the vector may be one which, when introduced in a host cell, is integrated in the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

Expression vectors may be constructed to include any of the
20 DNA segments disclosed herein. Such DNA might encode an antigenic protein specific for virulent strains of mycobacteria or even hybridization probes for detecting mycobacteria nucleic acids in samples. Longer or shorter DNA segments could be used, depending on the antigenic protein desired.
25 Epitopic regions of the proteins expressed or encoded by the disclosed DNA could be included as relatively short segments of DNA. A wide variety of expression vectors is possible including, for example, DNA segments encoding reporter gene products useful for identification of heterologous gene
30 products and/or resistance genes such as antibiotic resistance genes which may be useful in identifying transformed cells.

The vector of the invention may be used to transform cells so as to allow propagation of the nucleic acid fragments of the

invention or so as to allow expression of the polypeptide fragments of the invention. Hence, the invention also pertains to a transformed cell harbouring at least one such vector according to the invention, said cell being one which
5 does not natively harbour the vector and/or the nucleic acid fragment of the invention contained therein. Such a transformed cell (which is also a part of the invention) may be any suitable bacterial host cell or any other type of cell such as a unicellular eukaryotic organism, a fungus or yeast,
10 or a cell derived from a multicellular organism, e.g. an animal or a plant. It is especially in cases where glycosylation is desired that a mammalian cell is used, although glycosylation of proteins is a rare event in prokaryotes. Normally, however, a prokaryotic cell is preferred
15 such as a bacterium belonging to the genera *Mycobacterium*, *Salmonella*, *Pseudomonas*, *Bacillus* and *Eschericia*. It is preferred that the transformed cell is an *E. coli*, *B. subtilis*, or *M. bovis* BCG cell, and it is especially preferred that the transformed cell expresses a polypeptide according
20 of the invention. The latter opens for the possibility to produce the polypeptide of the invention by simply recovering it from the culture containing the transformed cell. In the most preferred embodiment of this part of the invention the transformed cell is *Mycobacterium bovis* BCG strain: Danish
25 1331, which is the *Mycobacterium bovis* strain Copenhagen from the Copenhagen BCG Laboratory, Statens Seruminstitut, Denmark.

The nucleic acid fragments of the invention allow for the recombinant production of the polypeptides fragments of the
30 invention. However, also isolation from the natural source is a way of providing the polypeptide fragments as is peptide synthesis.

Therefore, the invention also pertains to a method for the preparation of a polypeptide fragment of the invention, said
35 method comprising inserting a nucleic acid fragment as defined above into a vector which is able to replicate in a

host cell, introducing the resulting recombinant vector into the host cell (transformed cells may be selected using various techniques, including screening by differential hybridization, identification of fused reporter gene products, resistance markers, anti-antigen antibodies and the like),
5 culturing the host cell in a culture medium under conditions sufficient to effect expression of the polypeptide (of course the cell may be cultivated under conditions appropriate to the circumstances, and if DNA is desired, replication conditions are used), and recovering the polypeptide from the host
10 cell or culture medium; or

isolating the polypeptide from a short-term culture filtrate as defined in claim 1; or

isolating the polypeptide from whole mycobacteria of the
15 tuberculosis complex or from lysates or fractions thereof, e.g. cell wall containing fractions, or

synthesizing the polypeptide by solid or liquid phase peptide synthesis.

The medium used to grow the transformed cells may be any
20 conventional medium suitable for the purpose. A suitable vector may be any of the vectors described above, and an appropriate host cell may be any of the cell types listed above. The methods employed to construct the vector and effect introduction thereof into the host cell may be any
25 methods known for such purposes within the field of recombinant DNA. In the following a more detailed description of the possibilities will be given:

In general, of course, prokaryotes are preferred for the initial cloning of nucleic sequences of the invention and
30 constructing the vectors useful in the invention. For example, in addition to the particular strains mentioned in the more specific disclosure below, one may mention by way of example, strains such as *E. coli* K12 strain 294 (ATCC No.

31446), *E. coli* B, and *E. coli* X 1776 (ATCC No. 31537). These examples are, of course, intended to be illustrative rather than limiting.

Prokaryotes are also preferred for expression. The
5 aforementioned strains, as well as *E. coli* W3110 (F-, lambda-, prototrophic, ATCC No. 27325), bacilli such as *Bacillus subtilis*, or other enterobacteriaceae such as *Salmonella typhimurium* or *Serratia marcesans*, and various *Pseudomonas* species may be used. Especially interesting are rapid-growing
10 mycobacteria, e.g. *M. smegmatis*, as these bacteria have a high degree of resemblance with mycobacteria of the tuberculosis complex and therefore stand a good chance of reducing the need of performing post-translational modifications of the expression product.

15 In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection
20 in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species (see, e.g., Bolivar et al., 1977, Gene 2: 95). The pBR322 plasmid contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying
25 transformed cells. The pBR plasmid, or other microbial plasmid or phage must also contain, or be modified to contain, promoters which can be used by the microorganism for expression.

Those promoters most commonly used in recombinant DNA construction include the B-lactamase (penicillinase) and lactose
30 promoter systems (Chang et al., 1978; Itakura et al., 1977; Goeddel et al., 1979) and a tryptophan (*trp*) promoter system (Goeddel et al., 1979; EPO Appl. Publ. No. 0036776). While these are the most commonly used, other microbial promoters
35 have been discovered and utilized, and details concerning

their nucleotide sequences have been published, enabling a skilled worker to ligate them functionally with plasmid vectors (Siebwenlist et al., 1980). Certain genes from prokaryotes may be expressed efficiently in *E. coli* from their own promoter sequences, precluding the need for addition of another promoter by artificial means.

After the recombinant preparation of the polypeptide according to the invention, the isolation of the polypeptide may for instance be carried out by affinity chromatography (or other conventional biochemical procedures based on chromatography), using a monoclonal antibody which substantially specifically binds the polypeptide according to the invention. Another possibility is to employ the simultaneous electroelution technique described by Andersen et al. in J. Immunol. Methods **161**: 29-39.

According to the invention the post-translational modifications involves lipidation, glycosylation, cleavage, or elongation of the polypeptide.

In certain aspects, the DNA sequence information provided by this invention allows for the preparation of relatively short DNA (or RNA or PNA) sequences having the ability to specifically hybridize to mycobacterial gene sequences. In these aspects, nucleic acid probes of an appropriate length are prepared based on a consideration of the relevant sequence. The ability of such nucleic acid probes to specifically hybridize to the mycobacterial gene sequences lend them particular utility in a variety of embodiments. Most importantly, the probes can be used in a variety of diagnostic assays for detecting the presence of pathogenic organisms in a given sample. However, other uses are envisioned, including the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructs.

Apart from their use as starting points for the synthesis of polypeptides of the invention and for hybridization probes (useful for direct hybridization assays or as primers in e.g. PCR or other molecular amplification methods) the nucleic acid fragments of the invention may be used for effecting *in vivo* expression of antigens, *i.e.* the nucleic acid fragments may be used in so-called DNA vaccines. Recent research have revealed that a DNA fragment cloned in a vector which is non-replicative in eukaryotic cells may be introduced into an animal (including a human being) by e.g. intramuscular injection or percutaneous administration (the so-called "gene gun" approach). The DNA is taken up by e.g. muscle cells and the gene of interest is expressed by a promoter which is functioning in eukaryotes, e.g. a viral promoter, and the gene product thereafter stimulates the immune system. These newly discovered methods are reviewed in Ulmer et al., 1993, which hereby is included by reference.

Hence, the invention also relates to a vaccine comprising a nucleic acid fragment according to the invention, the vaccine effecting *in vivo* expression of antigen by an animal, including a human being, to whom the vaccine has been administered, the amount of expressed antigen being effective to confer substantially increased resistance to infections with mycobacteria of the tuberculosis complex in an animal, including a human being.

The efficacy of such a "DNA vaccine" can possibly be enhanced by administering the gene encoding the expression product together with a DNA fragment encoding a polypeptide which has the capability of modulating an immune response. For instance, a gene encoding lymphokine precursors or lymphokines (e.g. IFN- γ , IL-2, or IL-12) could be administered together with the gene encoding the immunogenic protein, either by administering two separate DNA fragments or by administering both DNA fragments included in the same vector. It also is a possibility to administer DNA fragments comprising a multitude of nucleotide sequences which each encode

relevant epitopes of the polypeptides disclosed herein so as to effect a continuous sensitization of the immune system with a broad spectrum of these epitopes.

As explained above, the polypeptide fragments of the invention are excellent candidates for vaccine constituents or for constituents in an immune diagnostic agent due to their extracellular presence in culture media containing metabolizing virulent mycobacteria belonging to the tuberculosis complex, or because of their high homologies with such extracellular antigens, or because of their absence in *M. bovis* BCG.

Thus, another part of the invention pertains to an immunologic composition comprising a polypeptide or fusion polypeptide according to the invention. In order to ensure optimum performance of such an immunologic composition it is preferred that it comprises an immunologically and pharmaceutically acceptable carrier, vehicle or adjuvant.

Suitable carriers are selected from the group consisting of a polymer to which the polypeptide(s) is/are bound by hydrophobic non-covalent interaction, such as a plastic, e.g. polystyrene, or a polymer to which the polypeptide(s) is/are covalently bound, such as a polysaccharide, or a polypeptide, e.g. bovine serum albumin, ovalbumin or keyhole limpet haemocyanin. Suitable vehicles are selected from the group consisting of a diluent and a suspending agent. The adjuvant is preferably selected from the group consisting of dimethyldioctadecylammonium bromide (DDA), Quil A, poly I:C, Freund's incomplete adjuvant, IFN- γ , IL-2, IL-12, monophosphoryl lipid A (MPL), and muramyl dipeptide (MDP).

A preferred immunologic composition according to the present invention comprising at least two different polypeptide fragments, each different polypeptide fragment being a polypeptide or a fusion polypeptide defined above. It is

preferred that the immunologic composition comprises between 3-20 different polypeptide fragments or fusion polypeptides.

Such an immunologic composition may preferably be in the form of a vaccine or in the form of a skin test reagent.

- 5 In line with the above, the invention therefore also pertain to a method for producing an immunologic composition according to the invention, the method comprising preparing, synthesizing or isolating a polypeptide according to the invention, and solubilizing or dispersing the polypeptide in
10 a medium for a vaccine, and optionally adding other *M. tuberculosis* antigens and/or a carrier, vehicle and/or adjuvant substance.

Preparation of vaccines which contain peptide sequences as active ingredients is generally well understood in the art,
15 as exemplified by U.S. Patents 4,608,251; 4,601,903; 4,599,231; 4,599,230; 4,596,792; and 4,578,770, all incorporated herein by reference. Typically, such vaccines are prepared as injectables either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension
20 in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredient is often mixed with excipients which are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline,
25 dextrose, glycerol, ethanol, or the like, and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants which enhance the effectiveness of the vaccines.

- 30 The vaccines are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional

binders and carriers may include, for example, polyalkalene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1-2%. Oral formulations include
5 such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release
10 formulations or powders and contain 10-95% of active ingredient, preferably 25-70%.

The proteins may be formulated into the vaccine as neutral or salt forms. Pharmaceutically acceptable salts include acid addition salts (formed with the free amino groups of the
15 peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic bases such as, for example, sodium,
20 potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective and immunogenic. The quantity to be administered depends on the subject to be treated, including, e.g.,
25 the capacity of the individual's immune system to mount an immune response, and the degree of protection desired. Suitable dosage ranges are of the order of several hundred
30 micrograms active ingredient per vaccination with a preferred range from about 0.1 μg to 1000 μg , such as in the range from about 1 μg to 300 μg , and especially in the range from about 10 μg to 50 μg . Suitable regimens for initial administration and booster shots are also variable but are typified by an
35 initial administration followed by subsequent inoculations or other administrations.

The manner of application may be varied widely. Any of the conventional methods for administration of a vaccine are applicable. These are believed to include oral application on a solid physiologically acceptable base or in a physiologically acceptable dispersion, parenterally, by injection or the like. The dosage of the vaccine will depend on the route of administration and will vary according to the age of the person to be vaccinated and, to a lesser degree, the size of the person to be vaccinated.

- 10 Some of the polypeptides of the vaccine are sufficiently immunogenic in a vaccine, but for some of the others the immune response will be enhanced if the vaccine further comprises an adjuvant substance.

Various methods of achieving adjuvant effect for the vaccine include use of agents such as aluminum hydroxide or phosphate (alum), commonly used as 0.05 to 0.1 percent solution in phosphate buffered saline, admixture with synthetic polymers of sugars (Carbopol) used as 0.25 percent solution, aggregation of the protein in the vaccine by heat treatment with temperatures ranging between 70° to 101°C for 30 second to 2 minute periods respectively. Aggregation by reactivating with pepsin treated (Fab) antibodies to albumin, mixture with bacterial cells such as C. parvum or endotoxins or lipopolysaccharide components of gram-negative bacteria, emulsion in physiologically acceptable oil vehicles such as mannide monooleate (Aracel A) or emulsion with 20 percent solution of a perfluorocarbon (Fluosol-DA) used as a block substitute may also be employed. According to the invention DDA (dimethyldioctadecylammonium bromide) is an interesting candidate for an adjuvant, but also Freund's complete and incomplete adjuvants as well as QuilA and RIBI are interesting possibilities. Further possibilities are monophosphoryl lipid A (MPL), and muramyl dipeptide (MDP).

Another highly interesting (and thus, preferred) possibility of achieving adjuvant effect is to employ the technique

described in Gosselin et al., 1992 (which is hereby incorporated by reference herein). In brief, the presentation of a relevant antigen such as an antigen of the present invention can be enhanced by conjugating the antigen to antibodies (or
5 antigen binding antibody fragments) against the Fc γ receptors on monocytes/macrophages. Especially conjugates between antigen and anti-Fc γ RI have been demonstrated to enhance immunogenicity for the purposes of vaccination.

Other possibilities involve the use of immune modulating
10 substances such as lymphokines (e.g. IFN- γ , IL-2 and IL-12) or synthetic IFN- γ inducers such as poly I:C in combination with the above-mentioned adjuvants. As discussed in example 3, it is contemplated that such mixtures of antigen and adjuvant will lead to superior vaccine formulations.

15 In many instances, it will be necessary to have multiple administrations of the vaccine, usually not exceeding six vaccinations, more usually not exceeding four vaccinations and preferably one or more, usually at least about three vaccinations. The vaccinations will normally be at from two
20 to twelve week intervals, more usually from three to five week intervals. Periodic boosters at intervals of 1-5 years, usually three years, will be desirable to maintain the desired levels of protective immunity. The course of the immunization may be followed by in vitro proliferation assays
25 of PBL (peripheral blood lymphocytes) co-cultured with ESAT-6 or ST-CF, and especially by measuring the levels of IFN- γ released from the primed lymphocytes. The assays may be performed using conventional labels, such as radionuclides, enzymes, fluorescers, and the like. These techniques are well
30 known and may be found in a wide variety of patents, such as U.S. Patent Nos. 3,791,932; 4,174,384 and 3,949,064, as illustrative of these types of assays.

Due to genetic variation, different individuals may react with immune responses of varying strength to the same
35 polypeptide. Therefore, the vaccine according to the inven-

tion may comprise several different polypeptides in order to increase the immune response. The vaccine may comprise two or more polypeptides, where all of the polypeptides are as defined above, or some but not all of the peptides may be derived from a bacterium belonging to the *M. tuberculosis* complex. In the latter example the polypeptides not necessarily fulfilling the criteria set forth above for polypeptides may either act due to their own immunogenicity or merely act as adjuvants. Examples of such interesting polypeptides are MPB64, MPT64, and MPB59, but any other substance which can be isolated from mycobacteria are possible candidates.

The vaccine may comprise 3-20 different polypeptides, such as 3-10 different polypeptides.

One reason for admixing the polypeptides of the invention with an adjuvant is to effectively activate a cellular immune response. However, this effect can also be achieved in other ways, for instance by expressing the effective antigen in a vaccine in a non-pathogenic microorganism. A well-known example of such a microorganism is *Mycobacterium bovis* BCG.

Therefore, another important aspect of the present invention is an improvement of the living BCG vaccine presently available, which is a vaccine for immunizing an animal, including a human being, against TB caused by mycobacteria belonging to the tuberculosis-complex, comprising as the effective component a microorganism, wherein one or more copies of a DNA sequence encoding a polypeptide as defined above has been incorporated into the genome of the microorganism in a manner allowing the microorganism to express and secrete the polypeptide.

In the present context the term "genome" refers to the chromosome of the microorganisms as well as extrachromosomally DNA or RNA, such as plasmids. It is, however, preferred that the DNA sequence of the present invention has been introduced into the chromosome of the non-pathogenic microorganism,

since this will prevent loss of the genetic material introduced.

It is preferred that the non-pathogenic microorganism is a bacterium, e.g. selected from the group consisting of the
5 genera *Mycobacterium*, *Salmonella*, *Pseudomonas* and *Eschericia*.
It is especially preferred that the non-pathogenic microorganism is *Mycobacterium bovis* BCG, such as *Mycobacterium bovis* BCG strain: Danish 1331.

The incorporation of one or more copies of a nucleotide
10 sequence encoding the polypeptide according to the invention
in a mycobacterium from a *M. bovis* BCG strain will enhance
the immunogenic effect of the BCG strain. The incorporation
of more than one copy of a nucleotide sequence of the invention
is contemplated to enhance the immune response even
15 more, and consequently an aspect of the invention is a vaccine
wherein at least 2 copies of a DNA sequence encoding a
polypeptide is incorporated in the genome of the microorganism,
such as at least 5 copies. The copies of DNA sequences
may either be identical encoding identical polypeptides or be
20 variants of the same DNA sequence encoding identical or
homologues of a polypeptide, or in another embodiment be
different DNA sequences encoding different polypeptides where
at least one of the polypeptides is according to the present
invention.

25 The living vaccine of the invention can be prepared by cultivating
a transformed non-pathogenic cell according to the invention,
and transferring these cells to a medium for a vaccine, and
optionally adding a carrier, vehicle and/or adjuvant substance.

30 The invention also relates to a method of diagnosing TB
caused by *Mycobacterium tuberculosis*, *Mycobacterium africanum*
or *Mycobacterium bovis* in an animal, including a human being,
comprising intradermally injecting, in the animal, a
polypeptide according to the invention or a skin test reagent

described above, a positive skin response at the location of injection being indicative of the animal having TB, and a negative skin response at the location of injection being indicative of the animal not having TB. A positive response is a skin reaction having a diameter of at least 5 mm, but larger reactions are preferred, such as at least 1 cm, 1.5 cm, and at least 2 cm in diameter. The composition used as the skin test reagent can be prepared in the same manner as described for the vaccines above.

- 10 In line with the disclosure above pertaining to vaccine preparation and use, the invention also pertains to a method for immunising an animal, including a human being, against TB caused by mycobacteria belonging to the tuberculosis complex, comprising administering to the animal the polypeptide of the invention, or a vaccine composition of the invention as described above, or a living vaccine described above. Preferred routes of administration are the parenteral (such as intravenous and intraarterially), intraperitoneal, intramuscular, subcutaneous, intradermal, oral, buccal, sublingual, nasal, rectal or transdermal route.

The protein ESAT-6 which is present in short-term culture filtrates from mycobacteria as well as the *esat-6* gene in the mycobacterial genome has been demonstrated to have a very limited distribution in other mycobacterial strains than *M. tuberculosis*, e.g. *esat-6* is absent in both BCG and the majority of mycobacterial species isolated from the environment, such as *M. avium* and *M. terrae*. It is believed that this is also the case for at least one of the antigens of the present invention and their genes and therefore, the diagnostic embodiments of the invention are especially well-suited for performing the diagnosis of on-going or previous infection with virulent mycobacterial strains of the tuberculosis complex, and it is contemplated that it will be possible to distinguish between 1) subjects (animal or human) which have been previously vaccinated with e.g. BCG vaccines or subjected to antigens from non-virulent mycobacteria and 2)

subjects which have or have had active infection with virulent mycobacteria.

A number of possible diagnostic assays and methods can be envisaged:

- 5 When diagnosis of previous or ongoing infection with virulent mycobacteria is the aim, a blood sample comprising mononuclear cells (*i.a.* T-lymphocytes) from a patient could be contacted with a sample of one or more polypeptides of the invention. This contacting can be performed *in vitro* and a
10 positive reaction could e.g. be proliferation of the T-cells or release cytokines such as γ -interferon into the extracellular phase (e.g. into a culture supernatant); a suitable *in vivo* test would be a skin test as described above. It is also conceivable to contact a serum sample from a subject to
15 contact with a polypeptide of the invention, the demonstration of a binding between antibodies in the serum sample and the polypeptide being indicative of previous or ongoing infection.

- The invention therefore also relates to an *in vitro* method
- 20 for diagnosing ongoing or previous sensitization in an animal or a human being with bacteria belonging to the tuberculosis complex, the method comprising providing a blood sample from the animal or human being, and contacting the sample from the animal with the polypeptide of the invention, a significant
25 release into the extracellular phase of at least one cytokine by mononuclear cells in the blood sample being indicative of the animal being sensitized. By the term "significant release" is herein meant that the release of the cytokine is significantly higher than the cytokine release from a blood
30 sample derived from a non-tuberculous subject (e.g. a subject which does not react in a traditional skin test for TB). Normally, a significant release is at least two times the release observed from such a sample.

Alternatively, a sample of a possibly infected organ may be contacted with an antibody raised against a polypeptide of the invention. The demonstration of the reaction by means of methods well-known in the art between the sample and the antibody will be indicative of ongoing infection. It is of course also a possibility to demonstrate the presence of anti-mycobacterial antibodies in serum by contacting a serum sample from a subject with at least one of the polypeptide fragments of the invention and using well-known methods for visualizing the reaction between the antibody and antigen.

Also a method of determining the presence of mycobacterial nucleic acids in an animal, including a human being, or in a sample, comprising administering a nucleic acid fragment of the invention to the animal or incubating the sample with the nucleic acid fragment of the invention or a nucleic acid fragment complementary thereto, and detecting the presence of hybridized nucleic acids resulting from the incubation (by using the hybridization assays which are well-known in the art), is also included in the invention. Such a method of diagnosing TB might involve the use of a composition comprising at least a part of a nucleotide sequence as defined above and detecting the presence of nucleotide sequences in a sample from the animal or human being to be tested which hybridize with the nucleic acid fragment (or a complementary fragment) by the use of PCR technique.

The fact that certain of the disclosed antigens are not present in *M. bovis* BCG but are present in virulent mycobacteria point them out as interesting drug targets; the antigens may constitute receptor molecules or toxins which facilitate the infection by the mycobacterium, and if such functionalities are blocked the infectivity of the mycobacterium will be diminished.

To determine particularly suitable drug targets among the antigens of the invention, the gene encoding at least one of the polypeptides of the invention and the necessary control

sequences can be introduced into avirulent strains of mycobacteria (e.g. BCG) so as to determine which of the polypeptides are critical for virulence. Once particular proteins are identified as critical for/contributory to virulence, anti-mycobacterial agents can be designed rationally to inhibit expression of the critical genes or to attack the critical gene products. For instance, antibodies or fragments thereof (such as Fab and (Fab')₂ fragments can be prepared against such critical polypeptides by methods known in the art and thereafter used as prophylactic or therapeutic agents. Alternatively, small molecules can be screened for their ability to selectively inhibit expression of the critical gene products, e.g. using recombinant expression systems which include the gene's endogenous promoter, or for their ability to directly interfere with the action of the target. These small molecules are then used as therapeutics or as prophylactic agents to inhibit mycobacterial virulence.

Alternatively, anti-mycobacterial agents which render a virulent mycobacterium avirulent can be operably linked to expression control sequences and used to transform a virulent mycobacterium. Such anti-mycobacterial agents inhibit the replication of a specified mycobacterium upon transcription or translation of the agent in the mycobacterium. Such a "newly avirulent" mycobacterium would constitute a superb alternative to the above described modified BCG for vaccine purposes since it would be immunologically very similar to a virulent mycobacterium compared to e.g. BCG.

Finally, a monoclonal or polyclonal antibody, which is specifically reacting with a polypeptide of the invention in an immuno assay, or a specific binding fragment of said antibody, is also a part of the invention. The production of such polyclonal antibodies requires that a suitable animal be immunized with the polypeptide and that these antibodies are subsequently isolated, suitably by immune affinity chromatography. The production of monoclonals can be effected by

methods well-known in the art, since the present invention provides for adequate amounts of antigen for both immunization and screening of positive hybridomas.

LEGENDS TO THE FIGURES

- 5 Fig. 1: Long term memory immune mice are very efficiently protected towards an infection with *M. tuberculosis*. Mice were given a challenge of *M. tuberculosis* and spleens were isolated at different time points. Spleen lymphocytes were stimulated *in vitro* with ST-CF and the release of IFN- γ investigated (panel A). The counts of CFU in the spleens of the two groups of mice are indicated in panel B. The memory immune mice control infection within the first week and produce large quantities of IFN- γ in response to antigens in ST-CF.
- 10
- 15 Fig. 2: T cells involved in protective immunity are predominantly directed to molecules from 6-12 and 17-38 kDa. Splenic T cells were isolated four days after the challenge with *M. tuberculosis* and stimulated *in vitro* with narrow molecular mass fractions of ST-CF. The release of IFN- γ was investigated
- 20

Fig. 3: Nucleotide sequence (SEQ ID NO: 1) of *cfp7*. The deduced amino acid sequence (SEQ ID NO: 2) of CFP7 is given in conventional one-letter code below the nucleotide sequence. The putative ribosome-binding site is written in underlined italics as are the putative -10 and -35 regions. Nucleotides written in bold are those encoding CFP7.

25

Fig. 4. Nucleotide sequence (SEQ ID NO: 3) of *cfp9*. The deduced amino acid sequence (SEQ ID NO: 4) of CFP9 is given in conventional one-letter code below the nucleotide sequence. The putative ribosome-binding site Shine Delgarno sequence is written in underlined italics as are the putative -10 and -35 regions. Nucleotides in bold writing are those

30

encoding CFP9. The nucleotide sequence obtained from the lambda 226 phage is double underlined.

Fig. 5: Nucleotide sequence of *mpt51*. The deduced amino acid sequence of MPT51 is given in a one-letter code below the nucleotide sequence. The signal is indicated in italics. the putative potential ribosome-binding site is underlined. The nucleotide difference and amino acid difference compared to the nucleotide sequence of MPB51 (Ohara et al., 1995) are underlined at position 780. The nucleotides given in italics are not present in *M. tuberculosis* H37Rv.

Fig. 6: the position of the purified antigens in the 2DE system have been determined and mapped in a reference gel. The newly purified antigens are encircled and the position of well-known proteins are also indicated.

15 EXAMPLE 1

Identification of single culture filtrate antigens involved in protective immunity

A group of efficiently protected mice was generated by infecting 8-12 weeks old female C57Bl/6j mice with 5×10^4 *M. tuberculosis* i.v. After 30 days of infection the mice were subjected to 60 days of antibiotic treatment with isoniazid and were then left for 200-240 days to ensure the establishment of resting long-term memory immunity. Such memory immune mice are very efficiently protected against a secondary infection (Fig. 1). Long lasting immunity in this model is mediated by a population of highly reactive CD4 cells recruited to the site of infection and triggered to produce large amounts of IFN- γ in response to ST-CF (Fig. 1) (Andersen et al. 1995).

30 We have used this model to identify single antigens recognized by protective T cells. Memory immune mice were reinfected with 1×10^6 *M. tuberculosis* i.v. and splenic

lymphocytes were harvested at day 4-6 of reinfection, a time point where this population is highly reactive to ST-CF. The antigens recognized by these T cells were mapped by the multi-elution technique (Andersen and Heron, 1993). This technique divides complex protein mixtures separated in SDS-PAGE into narrow fractions in a physiological buffer. These fractions were used to stimulate spleen lymphocytes *in vitro* and the release of IFN- γ was monitored (Fig. 2). Long-term memory immune mice did not recognize these fractions before TB infection, but splenic lymphocytes obtained during the recall of protective immunity recognized a range of culture filtrate antigens and peak production of IFN- γ was found in response to proteins of apparent molecular weight 6-12 and 17-30 kDa (Fig. 2). It is therefore concluded that culture filtrate antigens within these regions are the major targets recognized by memory effector T-cells triggered to release IFN- γ during the first phase of a protective immune response.

EXAMPLE 2

Cloning of genes expressing low mass culture filtrate antigens

In example 1 it was demonstrated that antigens in the low molecular mass fraction are recognized strongly by cells isolated from memory immune mice. Monoclonal antibodies (mAbs) to these antigens were therefore generated by immunizing with the low mass fraction in RIBI adjuvant (first and second immunization) followed by two injections with the fractions in aluminium hydroxide. Fusion and cloning of the reactive cell lines were done according to standard procedures (Kohler and Milstein 1975). The procedure resulted in the provision of two mAbs: ST-3 directed to a 9 kDa culture filtrate antigen (CFP9) and PV-2 directed to a 7 kDa antigen (CFP7), when the molecular weight is estimated from migration of the antigens in an SDS-PAGE.

In order to identify the antigens binding to the Mab's, the following experiments were carried out:

The recombinant λ gt11 *M. tuberculosis* DNA library constructed by R. Young (Young, R.A. et al. 1985) and obtained through
5 the World Health Organization IMMTUB programme (WHO.0032.wibr) was screened for phages expressing gene products which would bind the monoclonal antibodies ST-3 and PV-2.

Approximately 1×10^5 pfu of the gene library (containing
10 approximately 25% recombinant phages) were plated on *Escherichia coli* Y1090 (DlacU169, proA⁺, Dlon, araD139, supF, trpC22::tn10 [pMC9] ATCC#37197) in soft agar and incubated for 2,5 hours at 42°C.

The plates were overlaid with sheets of nitrocellulose saturated with isopropyl- β -D-thiogalactopyranoside and incubation
15 was continued for 2,5 hours at 37°C. The nitrocellulose was removed and incubated with samples of the monoclonal antibodies in PBS with Tween 20 added to a final concentration of 0.05%. Bound monoclonal antibodies were visualized by horse-
20 radish peroxidase-conjugated rabbit anti-mouse immunoglobulins (P260, Dako, Glostrup, DK) and a staining reaction involving 5,5',3,3'-tetramethylbenzidine and H₂O₂.

Positive plaques were recloned and the phages originating from a single plaque were used to lysogenize *E. coli* Y1089
25 (DlacU169, proA⁺, Dlon, araD139, strA, hfl150 [chr::tn10] [pMC9] ATCC nr. 37196). The resultant lysogenic strains were used to propagate phage particles for DNA extraction. These lysogenic *E. coli* strains have been named:

AA226 (expressing ST-3 reactive polypeptide CFP9) which has
30 been deposited 28 June 1993 with the collection of Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSM) under the accession number DSM 8377 and in accordance with the provisions of the Budapest Treaty, and

AA242 (expressing PV-2 reactive polypeptide CFP7) which has been deposited 28 June 1993 with the collection of Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSM) under the accession number DSM 8379 and in accordance with
5 the provisions of the Budapest Treaty.

These two lysogenic *E. coli* strains are disclosed in WO 95/01441 as are the mycobacterial polypeptide products expressed thereby. However, no information concerning the amino acid sequences of these polypeptides or their genetic
10 origin are given, and therefore only the direct expression products of AA226 and AA242 are made available to the public.

The st-3 binding protein is expressed as a protein fused to β -galactosidase, whereas the pv-2 binding protein appears to be expressed in an unfused version.

15 Sequencing of the nucleotide sequence encoding the PV-2 and ST-3 binding protein

In order to obtain the nucleotide sequence of the gene encoding the pv-2 binding protein, the approximately 3 kb *M. tuberculosis* derived *EcoRI* - *EcoRI* fragment from AA242 was
20 subcloned in the *EcoRI* site in the pBluescriptSK + (Stratagene) and used to transform *E. coli* XL-1Blue (Stratagene).

Similarly, to obtain the nucleotide sequence of the gene encoding the st-3 binding protein, the approximately 5 kb *M. tuberculosis* derived *EcoRI* - *EcoRI* fragment from AA226 was
25 subcloned in the *EcoRI* site in the pBluescriptSK + (Stratagene) and used to transform *E. coli* XL-1Blue (Stratagene).

The complete DNA sequence of both genes were obtained by the dideoxy chain termination method adapted for supercoiled DNA by use of the Sequenase DNA sequencing kit version 1.0
30 (United States Biochemical Corp., Cleveland, OH) and by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems)

according to the instructions provided. The sequences DNA are shown in SEQ ID NO: 1 (CFP7) and in SEQ ID NO: 3 (CFP9) as well as in Figs. 3 and 4, respectively. Both strands of the DNA were sequenced.

5 CFP7

An open reading frame (ORF) encoding a sequence of 96 amino acid residues was identified from an ATG start codon at position 91-93 extending to a TAG stop codon at position 379-381. The deduced amino acid sequence is shown in SEQ ID NO: 2
10 (and in Fig. 3 where conventional one-letter amino acid codes are used).

CFP7 appear to be expressed in *E. coli* as an unfused version. The nucleotide sequence at position 78-84 is expected to be the Shine Delgarno sequence and the sequences from position
15 47-50 and 14-19 are expected to be the -10 and -35 regions, respectively:

CFP9

The protein recognised by ST-3 was produced as a β -galactosidase fusion protein, when expressed from the AA226 lambda
20 phage. The fusion protein had an approx. size of 116 - 117kDa (Mw for β -galactosidase 116.25 kDa) which may suggest that only part of the CFP9 gene was included in the lambda clone (AA226).

Based on the 90 bp nucleotide sequence obtained on the insert
25 from lambda phage AA226, a search of homology to the nucleotide sequence of the *M. tuberculosis* genome was performed in the Sanger database (Sanger *Mycobacterium tuberculosis* database):

<http://www.sanger.ac.uk/pathogens/TB-blast-server.html>;

Williams, 1996). 100% identity to the cloned sequence was found on the MTCY48 cosmid. An open reading frame (ORF) encoding a sequence of 109 amino acid residues was identified from a GTG start codon at position 141 - 143 extending to a
5 TGA stop codon at position 465 - 467. The deduced amino acid sequence is shown in Fig. 4 using conventional one letter code.

The nucleotide sequence at position 123 - 130 is expected to be the Shine Delgarno sequence and the sequences from position 73 - 78 and 4 - 9 are expected to be the -10 and -35 region respectively (Fig. 4). The ORF overlapping with the
10 5'-end of the sequence of AA229 is shown in Fig. 4 by double underlining.

Subcloning CFP7 and CFP9 in expression vectors

15

The two ORFs encoding CFP7 and CFP9 were PCR cloned into the pMST24 (Theisen et al., 1995) expression vector pRVN01 or the pQE-32 (QIAGEN) expression vector pRVN02, respectively.

The PCR amplification was carried out in a thermal reactor
20 (Rapid cycler, Idaho Technology, Idaho) by mixing 10 ng plasmid DNA with the mastermix (0.5 μ M of each oligonucleotide primer, 0.25 μ M BSA (Stratagene), low salt buffer (20 mM Tris-HCl, pH 8.8, 10 mM KCl, 10 mM $(\text{NH}_4)_2\text{SO}_4$, 2 mM MgSO_4 and 0.1% Triton X-100) (Stratagene), 0.25 mM of each deoxynucleo-
25 side triphosphate and 0.5 U Taq Plus Long DNA polymerase (Stratagene)). Final volume was 10 μ l (all concentrations given are concentrations in the final volume). Predenaturation was carried out at 94°C for 30 s. 30 cycles of the following was performed; Denaturation at 94°C for 30 s,
30 annealing at 55°C for 30 s and elongation at 72°C for 1 min.

The oligonucleotide primers were synthesised automatically on a DNA synthesizer (Applied Biosystems, Foster City, Ca, ABI-391, PCR-mode), deblocked, and purified by ethanol precipitation.

The *cfp7* oligonucleotides (TABLE 1) were synthesised on the basis of the nucleotide sequence from the CFP7 sequence (Fig. 3). The oligonucleotides were engineered to include an *SmaI* restriction enzyme site at the 5' end and a *BamHI* restriction enzyme site at the 3' end for directed subcloning.

The *cfp9* oligonucleotides (TABLE 1) were synthesized partly on the basis of the nucleotide sequence from the sequence of the AA229 clone and partly from the identical sequence found in the Sanger database cosmid MTCY48 (Fig. 4). The oligonucleotides were engineered to include a *SmaI* restriction enzyme site at the 5' end and a *HindIII* restriction enzyme site at the 3' end for directed subcloning.

CFP7

By the use of PCR a *SmaI* site was engineered immediately 5' of the first codon of the ORF of 291 bp, encoding the *cfp7* gene, so that only the coding region would be expressed, and a *BamHI* site was incorporated right after the stop codon at the 3' end. The 291 bp PCR fragment was cleaved by *SmaI* and *BamHI*, purified from an agarose gel and subcloned into the *SmaI* - *BamHI* sites of the pMST24 expression vector. Vector DNA containing the gene fusion was used to transform the *E. coli* XL1-Blue (pRVN01).

CFP9

By the use of PCR a *SmaI* site was engineered immediately 5' of the first codon of an ORF of 327 bp, encoding the *cfp9* gene, so that only the coding region would be expressed, and a *HindIII* site was incorporated after the stop codon at the 3' end. The 327 bp PCR fragment was cleaved by *SmaI* and *HindIII*, purified from an agarose gel, and subcloned into the *SmaI* - *HindIII* sites of the pQE-32 (QIAGEN) expression vector. Vector DNA containing the gene fusion was used to transform the *E. coli* XL1-Blue (pRVN02).

Purification of recombinant CFP7 and CFP9

The ORFs were fused N-terminally to the (His)₆-tag (cf. EP-A-0 282 242). Recombinant antigen was prepared as follows: Briefly, a single colony of *E. coli* harbouring either the
5 pRVN01 or the pRVN02 plasmid, was inoculated into Luria-Bertani broth containing 100 µg/ml ampicillin and 12.5 µg/ml tetracycline and grown at 37°C to OD_{600nm} = 0.5. IPTG (isopropyl-β-D-thiogalactoside) was then added to a final concentration of 2 mM (expression was regulated either by the
10 strong IPTG inducible P_{tac} or the T5 promoter) and growth was continued for further 2 hours. The cells were harvested by centrifugation at 4,200 x g at 4°C for 8 min. The pelleted bacteria were stored overnight at -20°C. The pellet was resuspended in BC 40/100 buffer (20 mM Tris-HCl pH 7.9, 20%
15 glycerol, 100 mM KCl, 40 mM Imidazole) and cells were broken by sonication (5 times for 30 s with intervals of 30 s) at 4°C. followed by centrifugation at 12,000 x g for 30 min at 4°C, the supernatant (crude extract) was used for purification of the recombinant antigens.

20 The two Histidine fusion proteins (His-rCFP7 and His-rCFP9) were purified from the crude extract by affinity chromatography on a Ni²⁺-NTA column from QIAGEN with a volume of 100 ml. His-rCFP7 and His-rCFP9 binds to Ni²⁺. After extensive washes of the column in BC 40/100 buffer, the fusion protein
25 was eluted with a BC 1000/100 buffer containing 100 mM imidazole, 20 mM Tris pH 7.9, 20% glycerol and 1 M KCl. subsequently, the purified products were dialysed extensively against 10 mM Tris pH 8.0. His-rCFP7 and His-rCFP9 were then separated from contaminants by fast protein liquid chromatography (FPLC) over an anion-exchange column (Mono Q, Pharmacia, Sweden). in 10 mM Tris pH 8.0 with a linear gradient of
30 NaCl from 0 to 1 M. Aliquots of the fractions were analyzed by 10%-20% gradient sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE). Fractions containing purified
35 either purified His-rCFP7 or His-rCFP9 were pooled.

TABLE 1. Sequence of the *cfp7* and *cfp9* oligonucleotides^a.

Orientation and oligonucleotide	Sequences (5' → 3')	Position ^b (nucleotide)
Sense		
5 pvr3	<u>GCAACACCCGGG</u> ATGTCGCAAATCATG (SEQ ID NO: 43)	91-105 (SEQ ID NO: 1)
str2	<u>GTAACACCCGGG</u> TGGCCGCCGACCCG (SEQ ID NO: 44)	141-155 (SEQ ID NO: 3)
Antisense		
pvF4	CTACTAAGCTTGGATCCCTAGCCGCCCATTTGGCGG (SEQ ID NO: 45)	381-362 (SEQ ID NO: 1)
stF2	CTACTAAGCTTCCATGGTCAGGTCTTTTCGATGCTTAC (SEQ ID NO: 46)	467 - 447 (SEQ ID NO: 3)

10 ^a The *cfp7* oligonucleotides were based on the nucleotide sequence shown in Fig. 3 (SEQ ID NO: 1). The *cfp9* oligonucleotides were based on the nucleotide sequence shown in Fig. 4 (SEQ ID NO: 3). Nucleotides underlined are not contained in the nucleotide sequence of *cfp7* and *cfp9*.

15 ^b The positions referred to are of the non-underlined part of the primers and correspond to the nucleotide sequence shown in Fig. 3 and Fig. 4, respectively.

EXAMPLE 2A

20 Identification of antigens which are not expressed in BCG strains.

In an effort to control the treat of TB, attenuated bacillus Calmette-Guérin (BCG) has been used as a live attenuated vaccine. BCG is an attenuated derivative of a virulent *Mycobacterium bovis*. The original BCG from the Pasteur Institute in Paris, France was developed from 1908 to 1921 by 231 passages in liquid culture and has never been shown to revert to virulence in animals, indicating that the attenuating mutation(s) in BCG are stable deletions and/or multiple mutations which do not readily revert. While physiological differences between BCG and *M. tuberculosis* and *M. bovis* has been noted, the attenuating mutations which arose during serial passage of the original BCG strain has been unknown until recently. The first mutations described are the loss of the gene encoding MPB64 in some BCG strains (Li et al., 1993, Oettinger and Andersen, 1994) and the gene encoding ESAT-6 in all BCG strain tested (Harboe et al., 1996), later 3 large deletions in BCG have been identified (Mahairas et al., 1996). The region named RD1 includes the gene encoding ESAT-6

and an other (RD2) the gene encoding MPT64. Both antigens have been shown to have diagnostic potential and ESAT-6 has been shown to have properties as a vaccine candidate (cf. PCT/DK94/00273 and PCT/DK/00270). In order to find new *M. tuberculosis* specific diagnostic antigens as well as antigens for a new vaccine against TB, the RD1 region (17.499 bp) of *M. tuberculosis* H37Rv has been analyzed for Open Reading Frames (ORF). ORFs with a minimum length of 96 bp have been predicted using the algorithm described by Borodovsky and McIninch (1993), in total 27 ORFs have been predicted, 20 of these have possible diagnostic and/or vaccine potential, as they are deleted from all known BCG strains. The predicted ORFs include ESAT-6 (RD1-ORF7) and CFP10 (RD1-ORF6) described previously (Sørensen et al., 1995), as a positive control for the ability of the algorithm. In the present is described the potential of 7 of the predicted antigens for diagnosis of TB as well as potential as candidates for a new vaccine against TB.

Seven open reading frames (ORF) from the 17,499kb RD1 region (Accession no. U34848) with possible diagnostic and vaccine potential have been identified and cloned.

Identification of the ORF's *rd1-orf2*, *rd1-orf3*, *rd1-orf4*, *rd1-orf5*, *rd1-orf8*, *rd1-orf9a*, and *rd1-orf9b*.

The nucleotide sequence of *rd1-orf2* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 71. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 72.

The nucleotide sequence of *rd1-orf3* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 87. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 88.

The nucleotide sequence of *rd1-orf4* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 89. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 90.

The nucleotide sequence of *rd1-orf5* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 91. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 92.

5 The nucleotide sequence of *rd1-orf8* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 67. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 68.

The nucleotide sequence of *rd1-orf9a* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 93. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 94.

10 The nucleotide sequence of *rd1-orf9b* from *M. tuberculosis* H37Rv is set forth in SEQ ID NO: 69. The deduced amino acid sequence of RD1-ORF2 is set forth in SEQ ID NO: 70.

The DNA sequence *rd1-orf2* (SEQ ID NO: 71) contained an open reading frame starting with an ATG codon at position 889 -
15 891 and ending with a termination codon (TAA) at position 2662 - 2664 (position numbers referring to the location in RD1). The deduced amino acid sequence (SEQ ID NO: 72) contains 591 residues corresponding to a molecular weight of 64,525.

20 The DNA sequence *rd1-orf3* (SEQ ID NO: 87) contained an open reading frame starting with an ATG codon at position 2807 - 2809 and ending with a termination codon (TAA) at position 3101 - 3103 (position numbers referring to the location in RD1). The deduced amino acid sequence (SEQ ID NO: 88) con-
25 tains 98 residues corresponding to a molecular weight of 9,799.

The DNA sequence *rd1-orf4* (SEQ ID NO: 89) contained an open reading frame starting with a GTG codon at position 4014 - 4012 and ending with a termination codon (TAG) at position
30 3597 - 3595 (position numbers referring to the location in RD1). The deduced amino acid sequence (SEQ ID NO: 90) con-

tains 139 residues corresponding to a molecular weight of 14,210.

The DNA sequence rd1-orf5 (SEQ ID NO: 91) contained an open reading frame starting with a GTG codon at position 3128 -
5 3130 and ending with a termination codon (TGA) at position 4241 - 4243 (position numbers referring to the location in RD1). The deduced amino acid sequence (SEQ ID NO: 92) contains 371 residues corresponding to a molecular weight of 37,647.

10 The DNA sequence rd1-orf8 (SEQ ID NO: 67) contained an open reading frame starting with a GTG codon at position 5502 - 5500 and ending with a termination codon (TAG) at position 5084 - 5082 (position numbers referring to the location in RD1), and the deduced amino acid sequence (SEQ ID NO: 68)
15 contains 139 residues with a molecular weight of 11,737.

The DNA sequence rd1-orf9a (SEQ ID NO: 93) contained an open reading frame starting with a GTG codon at position 6146 - 6148 and ending with a termination codon (TAA) at position 7070 - 7072 (position numbers referring to the location in
20 RD1). The deduced amino acid sequence (SEQ ID NO: 94) contains 308 residues corresponding to a molecular weight of 33,453.

The DNA sequence rd1-orf9b (SEQ ID NO: 69) contained an open reading frame starting with an ATG codon at position 5072 -
25 5074 and ending with a termination codon (TAA) at position 7070 - 7072 (position numbers referring to the location in RD1). The deduced amino acid sequence (SEQ ID NO: 70) contains 666 residues corresponding to a molecular weight of 70,650.

Cloning of the ORF's *rdl-orf2*, *rdl-orf3*, *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a*, and *rdl-orf9b*.

The ORF's *rdl-orf2*, *rdl-orf3*, *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a* and *rdl-orf9b* were PCR cloned in the pMST24 (Thei-
sen et al., 1995) (*rdl-orf3*) or the pQE32 (QIAGEN) (*rdl-orf2*,
5 *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a* and *rdl-orf9b*) ex-
pression vector. Preparation of oligonucleotides and PCR
amplification of the *rdl-orf* encoding genes, was carried out
as described in example 2. Chromosomal DNA from *M. tuberculo-*
10 *sis* H37Rv was used as template in the PCR reactions. Oligonu-
cleotides were synthesized on the basis of the nucleotide
sequence from the RD1 region (Accession no. U34848). The
oligonucleotide primers were engineered to include an re-
striction enzyme site at the 5' end and at the 3' end by
15 which a later subcloning was possible. Primers are listed in
TABLE 2.

rdl-orf2. A *Bam*HI site was engineered immediately 5' of the
first codon of *rdl-orf2*, and a *Hind*III site was incorporated
right after the stop codon at the 3' end. The gene *rdl-orf2*
20 was subcloned in pQE32, giving pT096.

rdl-orf3. A *Sma*I site was engineered immediately 5' of the
first codon of *rdl-orf3*, and a *Nco*I site was incorporated
right after the stop codon at the 3' end. The gene *rdl-orf3*
was subcloned in pMST24, giving pT087.

25 *rdl-orf4*. A *Bam*HI site was engineered immediately 5' of the
first codon of *rdl-orf4*, and a *Hind*III site was incorporated
right after the stop codon at the 3' end. The gene *rdl-orf4*
was subcloned in pQE32, giving pT089.

30 *rdl-orf5*. A *Bam*HI site was engineered immediately 5' of the
first codon of *rdl-orf5*, and a *Hind*III site was incorporated
right after the stop codon at the 3' end. The gene *rdl-orf5*
was subcloned in pQE32, giving pT088.

rd1-orf8. A *Bam*HI site was engineered immediately 5' of the first codon of *rd1-orf8*, and a *Nco*I site was incorporated right after the stop codon at the 3' end. The gene *rd1-orf8* was subcloned in pMST24, giving pTO98.

- 5 *rd1-orf9a*. A *Bam*HI site was engineered immediately 5' of the first codon of *rd1-orf9a*, and a *Hind*III site was incorporated right after the stop codon at the 3' end. The gene *rd1-orf9a* was subcloned in pQE32, giving pTO91.

- 10 *rd1-orf9b*. A *Sca*I site was engineered immediately 5' of the first codon of *rd1-orf9b*, and a *Hind* III site was incorporated right after the stop codon at the 3' end. The gene *rd1-orf9b* was subcloned in pQE32, giving pTO90.

- 15 The PCR fragments were digested with the suitable restriction enzymes, purified from an agarose gel and cloned into either pMST24 or pQE-32. The seven constructs were used to transform the *E. coli* XL1-Blue. Endpoints of the gene fusions were determined by the dideoxy chain termination method. Both strands of the DNA were sequenced.

- 20 Purification of recombinant RD1-ORF2, RD1-ORF3, RD1-ORF4, RD1-ORF5, RD1-ORF8, RD1-ORF9a and RD1-ORF9b.

- The rRD1-ORFs were fused N-terminally to the (His)₆ -tag. Recombinant antigen was prepared as described in example 2 (with the exception that pTO91 was expressed at 30°C and not
25 at 37°C), using a single colony of *E. coli* harbouring either the pTO87, pTO88, pTO89, pTO90, pTO91, pTO96 or pTO98 for inoculation. Purification of recombinant antigen by Ni²⁺ affinity chromatography was also carried out as described in example 2. Fractions containing purified His-rRD1-ORF2, His-
30 rRD1-ORF3 His-rRD1-ORF4, His-rRD1-ORF5, His-rRD1-ORF8, His-rRD1-ORF9a or His-rRD1-ORF9b were pooled. The His-rRD1-ORF's were extensively dialysed against 10 mM Tris/HCl, pH 8.5, 3 M urea followed by an additional purification step performed on an anion exchange column (Mono Q) using fast protein liquid

chromatography (FPLC) (Pharmacia, Uppsala, Sweden). The purification was carried out in 10 mM Tris/HCl, pH 8.5, 3 M urea and protein was eluted by a linear gradient of NaCl from 0 to 1 M. Fractions containing the His-rRD1-ORF's were pooled and subsequently dialysed extensively against 25 mM Hepes, pH 8.0 before use.

Table 2. Sequence of the *rdl-orf's* oligonucleotides^a.

	Orientation and oligonucleotide	Sequences (5'→ 3')	Position (nt)
10	Sense		
	RD1-ORF2f	<u>CTGGGGATCC</u> GCATGACTGCTGAACCG	886 - 903
	RD1-ORF3f	<u>CTTCCCCGGG</u> ATGGAAAAAATGTCAC	2807 - 2822
	RD1-ORF4f	<u>GTAGGATCCTAG</u> GAGACATCAGCGGC	4028 - 4015
	RD1-ORF5f	<u>CTGGGGATCCG</u> CGTGATCACCATGCTGTGG	3028 - 3045
15	RD1-ORF8f	<u>CTCGGATCCTG</u> TGGGTGCAGGTCCGGCGATGGGC	5502 - 5479
	RD1-ORF9af	<u>GTGATGTGAGCT</u> CAGGTGAAGAAGGTGAAG	6144 - 6160
	RD1-ORF9bf	<u>GTGATGTGAGCTC</u> CTATGGCGGCCGACTACGAC	5072 - 5089
	Antisense		
	RD1-ORF2r	<u>TGCAAGCTTT</u> TAACCGGCGCTTGGGGGTGC	2664 - 2644
20	RD1-ORF3r	<u>GATGCCATGGT</u> TAGGCGAAGACGCCGGC	3103 - 3086
	RD1-ORF4r	<u>CGATCTAAGCT</u> TGGCAATGGAGGTCTA	3582 - 3597
	RD1-ORF5r	<u>TGCAAGCTTT</u> CACCAGTCGTCCTCTTCGTC	4243 - 4223
	RD1-ORF8r	<u>CTCCCATGGCT</u> ACGACAAGCTCTTCCGGCCGC	5083 - 5105
	RD1-ORF9a/br	<u>CGATCTAAGCTT</u> TCAACGACGTCCAGCC	7073 - 7056

^a The oligonucleotides were constructed from the Accession number U34484 nucleotide sequence (Mahairas et al., 1996). Nucleotides (nt) underlined are not contained in the nucleotide sequence of RD1-ORF's. The positions correspond to the nucleotide sequence of Accession number U34484.

The nucleotide sequences of *rdl-orf2*, *rdl-orf3*, *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a*, and *rdl-orf9b* from *M. tuberculosis* H37Rv are set forth in SEQ ID NO: 71, 87, 89, 91, 67, 93, and 69, respectively. The deduced amino acid sequences of *rdl-orf2*, *rdl-orf3*, *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a*, and *rdl-orf9b* are set forth in SEQ ID NO: 72, 88, 90, 92, 68, 94, and 70, respectively.

EXAMPLE 3

Cloning of the genes expressing 17-30 kDa antigens from ST-CF

Isolation of CFP17, CFP20, CFP21, CFP22, CFP25, and CFP28

ST-CF was precipitated with ammonium sulphate at 80% saturation. The precipitated proteins were removed by
5 centrifugation and after resuspension washed with 8 M urea. CHAPS and glycerol were added to a final concentration of 0.5% (w/v) and 5% (v/v) respectively and the protein solution was applied to a Rotofor isoelectrical Cell (BioRad). The
10 Rotofor Cell had been equilibrated with an 8 M urea buffer containing 0.5% (w/v) CHAPS, 5% (v/v) glycerol, 3% (v/v) Biolyt 3/5 and 1% (v/v) Biolyt 4/6 (BioRad). Isoelectric focusing was performed in a pH gradient from 3-6. The fractions were analyzed on silver-stained 10-20% SDS-PAGE. Fractions
15 with similar band patterns were pooled and washed three times with PBS on a Centriprep concentrator (Amicon) with a 3 kDa cut off membrane to a final volume of 1-3 ml. An equal volume of SDS containing sample buffer was added and the protein solution boiled for 5 min before further separation
20 on a Prep Cell (BioRad) in a matrix of 16% polyacrylamide under an electrical gradient. Fractions containing pure proteins with an molecular mass from 17-30 kDa were collected.

Isolation of CFP29

25 Anti-CFP29, reacting with CFP29 was generated by immunization of BALB/c mice with crushed gel pieces in RIBI adjuvant (first and second immunization) or aluminium hydroxide (third immunization and boosting) with two week intervals. SDS-PAGE gel pieces containing 2-5 µg of CFP29 were used for each
30 immunization. Mice were boosted with antigen 3 days before removal of the spleen. Generation of a monoclonal cell line producing antibodies against CFP29 was obtained essentially as described by Köhler and Milstein (1975). Screening of

5 supernatants from growing clones was carried out by immune blotting of nitrocellulose strips containing ST-CF separated by SDS-PAGE. Each strip contained approximately 50 μ g of ST-CF. The antibody class of anti-CFP29 was identified as IgM by the mouse monoclonal antibody isotyping kit, RPN29 (Amersham) according to the manufacturer's instructions.

CFP29 was purified by the following method: ST-CF was concentrated 10 fold by ultrafiltration, and ammonium sulphate precipitation in the 45 to 55% saturation range was performed. The pellet was redissolved in 50 mM sodium phosphate, 1.5 M ammonium sulphate, pH 8.5, and subjected to thiophilic adsorption chromatography (Porath et al., 1985) on an Affi-T gel column (Kem-En-Tec). Protein was eluted by a linear 1.5 to 0 M gradient of ammonium sulphate and fractions collected in the range 0.44 to 0.31 M ammonium sulphate were identified as CFP29 containing fractions in Western blot experiments with mAb Anti-CFP29. These fractions were pooled and anion exchange chromatography was performed on a Mono Q HR 5/5 column connected to an FPLC system (Pharmacia). The column was equilibrated with 10 mM Tris-HCl, pH 8.5 and the elution was performed with a linear gradient from 0 to 500 mM NaCl. From 400 to 500 mM sodium chloride, rather pure CFP29 was eluted. As a final purification step the Mono Q fractions containing CFP29 were loaded on a 12.5% SDS-PAGE gel and pure CFP29 was obtained by the multi-elution technique (Andersen and Heron, 1993).

N-terminal sequencing and amino acid analysis

CFP17, CFP20, CFP21, CFP22, CFP25, and CFP28 were washed with water on a Centricon concentrator (Amicon) with cutoff at 10 kDa and then applied to a ProSpin concentrator (Applied Biosystems) where the proteins were collected on a PVDF membrane. The membrane was washed 5 times with 20% methanol before sequencing on a Procise sequencer (Applied Biosystems).

CFP29 containing fractions were blotted to PVDF membrane after tricine SDS-PAGE (Ploug et al., 1989). The relevant bands were excised and subjected to amino acid analysis (Barkholt and Jensen, 1989) and N-terminal sequence analysis on a Procise sequencer (Applied Biosystems).

The following N-terminal sequences were obtained:

	For CFP17: A/S E L D A P A Q A G T E X A V	(SEQ ID NO: 17)
	For CFP20: A Q I T L R G N A I N T V G E	(SEQ ID NO: 18)
	For CFP21: D P X S D I A V V F A R G T H	(SEQ ID NO: 19)
10	For CFP22: T N S P L A T A T A T L H T N	(SEQ ID NO: 20)
	For CFP25: A X P D A E V V F A R G R F E	(SEQ ID NO: 21)
	For CFP28: X I/V Q K S L E L I V/T V/F T A D/Q E	(SEQ ID NO: 22)
	For CFP29: M N N L Y R D L A P V T E A A W A E I	(SEQ ID NO: 23)

"X" denotes an amino acid which could not be determined by the sequencing method used, whereas a "/" between two amino acids denotes that the sequencing method could not determine which of the two amino acids is the one actually present.

Cloning the gene encoding CFP29

The N-terminal sequence of CFP29 was used for a homology search in the EMBL database using the TFASTA program of the Genetics Computer Group sequence analysis software package. The search identified a protein, Linocin M18, from *Brevibacterium linens* that shares 74% identity with the 19 N-terminal amino acids of CFP29.

Based on this identity between the N-terminal sequence of CFP29 and the sequence of the Linocin M18 protein from *Brevibacterium linens*, a set of degenerated primers were constructed for PCR cloning of the *M. tuberculosis* gene encoding CFP29. PCR reactions were containing 10 ng of *M. tuberculosis* chromosomal DNA in 1 × low salt Taq+ buffer from Stratagene supplemented with 250 µM of each of the four nucleotides (Boehringer Mannheim), 0,5 mg/ml BSA (IgG technology), 1% DMSO (Merck), 5 pmoles of each primer and 0.5 unit Taq+ DNA polymerase (Stratagene) in 10 µl reaction volume. Reactions

were initially heated to 94°C for 25 sec. and run for 30 cycles of the program; 94°C for 15 sec., 55°C for 15 sec. and 72°C for 90 sec, using thermocycler equipment from Idaho Technology.

- 5 An approx. 300 bp fragment was obtained using primers with the sequences:

1: 5'-CCCGGCTCGAGAACCTSTACCGCGACCTSGCSCC (SEQ ID NO: 24)

2: 5'-GGGCCGGATCCGASGCSGCGTCCTTSACSGGYTGCCA (SEQ ID NO: 25)

-where S = G/C and Y = T/C

- 10 The fragment was excised from a 1% agarose gel, purified by Spin-X spin columns (Costar), cloned into pBluescript SK II+ - T vector (Stratagene) and finally sequenced with the Sequenase kit from United States Biochemical.

- 15 The first 150 bp of this sequence was used for a homology search using the Blast program of the Sanger *Mycobacterium tuberculosis* database:

(http://www.sanger.ac.uk/projects/M-tuberculosis/blast_server).

- 20 This program identified a *Mycobacterium tuberculosis* sequence on cosmid cy444 in the database that is nearly 100% identical to the 150 bp sequence of the CFP29 protein. The sequence is contained within a 795 bp open reading frame of which the 5' end translates into a sequence that is 100% identical to the N-terminally sequenced 19 amino acids of the purified CFP29 protein.

- 25 Finally, the 795 bp open reading frame was PCR cloned under the same PCR conditions as described above using the primers:

3: 5'-GGAAGCCCCATATGAACAATCTCTACCG (SEQ ID NO: 26)

4: 5'-CGCGCTCAGCCCTTAGTGACTGAGCGCGACCG (SEQ ID NO: 27)

The resulting DNA fragments were purified from agarose gels as described above sequenced with primer 3 and 4 in addition to the following primers:

- 5: 5'-GGACGTTCAAGCGACACATCGCCG-3' (SEQ ID NO: 115)
5 6: 5'-CAGCACGAACGCGCCGTCGATGGC-3' (SEQ ID NO: 116)

Three independent clones were sequenced. All three clones were in 100% agreement with the sequence on cosmid cy444.

All other DNA manipulations were done according to Maniatis et al. (1989).

- 10 All enzymes other than Taq polymerase were from New England Biolabs.

Homology searches in the Sanger database

- For CFP17, CFP20, CFP21, CFP22, CFP25, and CFP28 the N-terminal amino acid sequence from each of the proteins were used
15 for a homology search using the blast program of the Sanger *Mycobacterium tuberculosis* database:

<http://www.sanger.ac.uk/pathogens/TB-blast-server.html>.

- For CFP29 the first 150 bp of the DNA sequence was used for the search. Furthermore, the EMBL database was searched for
20 proteins with homology to CFP29.

Thereby, the following information were obtained:

CFP17

- Of the 14 determined amino acids in CFP17 a 93% identical sequence was found with MTCY1A11.16c. The difference between
25 the two sequences is in the first amino acid: It is an A or an S in the N-terminal determined sequenced and a S in

MTCY1A11. From the N-terminal sequencing it was not possible to determine amino acid number 13.

Within the open reading frame the translated protein is 162 amino acids long. The N-terminal of the protein purified from culture filtrate starts at amino acid 31 in agreement with the presence of a signal sequence that has been cleaved off. This gives a length of the mature protein of 132 amino acids, which corresponds to a theoretical molecular mass of 13833 Da and a theoretical pI of 4.4. The observed mass in SDS-PAGE is 17 kDa.

CFP20

A sequence 100% identical to the 15 determined amino acids of CFP20 was found on the translated cosmid cscy09F9. A stop codon is found at amino acid 166 from the amino acid M at position 1. This gives a predicted length of 165 amino acids, which corresponds to a theoretical molecular mass of 16897 Da and a pI of 4.2. The observed molecular weight in a SDS-PAGE is 20 kDa.

Searching the GenEMBL database using the TFASTA algorithm (Pearson and Lipman, 1988) revealed a number of proteins with homology to the predicted 164 amino acids long translated protein.

The highest homology, 51.5% identity in a 163 amino acid overlap, was found to a Haemophilus influenza Rd toxR reg. (HIHI0751).

CFP21

A sequence 100% identical to the 14 determined amino acids of CFP21 was found at MTCY39. From the N-terminal sequencing it was not possible to determine amino acid number 3; this amino acid is a C in MTCY39. The amino acid C can not be detected

on a Sequencer which is probably the explanation of this difference.

Within the open reading frame the translated protein is 217 amino acids long. The N-terminally determined sequence from
5 the protein purified from culture filtrate starts at amino acid 33 in agreement with the presence of a signal sequence that has been cleaved off. This gives a length of the mature protein of 185 amino acids, which corresponds to a theoretical molecular weight at 18657 Da, and a theoretical pI at 4,6.
10 The observed weight in a SDS-PAGE is 21 kDa.

In a 193 amino acids overlap the protein has 32,6% identity to a cutinase precursor with a length of 209 amino acids (CUTI_ALTBR P41744).

A comparison of the 14 N-terminal determined amino acids with
15 the translated region (RD2) deleted in *M. bovis* BCG revealed a 100% identical sequence (mb3484) (Mahairas et al. (1996)).

CFP22

A sequence 100% identical to the 15 determined amino acids of CFP22 was found at MTCY10H4. Within the open reading frame
20 the translated protein is 182 amino acids long. The N-terminal sequence of the protein purified from culture filtrate starts at amino acid 8 and therefore the length of the protein occurring in *M. tuberculosis* culture filtrate is 175 amino acids. This gives a theoretical molecular weight at
25 18517 Da and a pI at 6.8. The observed weight in a SDS-PAGE is 22 kDa.

In an 182 amino acids overlap the translated protein has 90,1% identity with E235739; a peptidyl-prolyl cis-trans isomerase.

CFP25

A sequence 93% identical to the 15 determined amino acids was found on the cosmid MTCY339.08c. The one amino acid that differs between the two sequences is a C in MTCY339.08c and a X from the N-terminal sequence data. On a Sequencer a C can not be detected which is a probable explanation for this difference.

The N-terminally determined sequence from the protein purified from culture filtrate begins at amino acid 33 in agreement with the presence of a signal sequence that has been cleaved off. This gives a length of the mature protein of 187 amino acids, which corresponds to a theoretical molecular weight at 19665 Da, and a theoretical pI at 4.9. The observed weight in a SDS-PAGE is 25 kDa.

In a 217 amino acids overlap the protein has 42.9% identity to CFP21 (MTCY39.35).

CFP28

No homology was found when using the 10 determined amino acid residues 2-8, 11, 12, and 14 of SEQ ID NO: 22 in the database search.

CFP29

Sanger database searching: A sequence nearly 100% identical to the 150 bp sequence of the CFP29 protein was found on cosmid cy444. The sequence is contained within a 795 bp open reading frame of which the 5' end translates into a sequence that is 100% identical to the N-terminally sequenced 19 amino acids of the purified CFP29 protein. The open reading frame encodes a 265 amino acid protein.

The amino acid analysis performed on the purified protein further confirmed the identity of CFP29 with the protein encoded in open reading frame on cosmid 444.

EMBL database searching: The open reading frame encodes a 265 amino acid protein that is 58% identical and 74% similar to the Linocin M18 protein (61% identity on DNA level). This is a 28.6 kDa protein with bacteriocin activity (Valdés-Stauber and Scherer, 1994; Valdés-Stauber and Scherer, 1996). The two proteins have the same length (except for 1 amino acid) and share the same theoretical physicochemical properties. We therefore suggest that CFP29 is a mycobacterial homolog to the *Brevibacterium linens* Linocin M18 protein.

The amino acid sequences of the purified antigens as picked from the Sanger database are shown in the following list. The amino acids determined by N-terminal sequencing are marked with bold.

CFP17 (SEQ ID NO: 6):

```

1  MTDMNPDI EK DQTSDEVTVE TTSVFRADFL SELDAPAQAG TESAVSGVEG
51  LPPGSALLV V KRGPNAGSRF LLDQAITSAG RHPDSDIFLD DVTVSRRHAE
20 101  FRLENNEFNV VDVGSLNGTY VNREPVDSAV LANGDEVQIG KFRLVFLTGP
151  KQGEDDGSTG GP

```

CFP20 (SEQ ID NO: 8):

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1  MAQITLRGNA INTVGELPAV GSPAPAFTLT GGD LGVISSD QFRGKSVLLN
51  IFPSVDTPVC ATSVRTFDER AAASGATVLC VSKDLPPFAQK RFCGAEGTEN
25 101  VMPASAFRDS FGEDYGV TIA DGPMAGLLAR AIVVIGADGN VAYTELVPEI
151  AQEPNYEAL AALGA

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CFP21 (SEQ ID NO: 10):

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1  MTPRSLVRIV GVVVATT LAL VSAPAGGRAA HADPCSDIAV
41  VFARGTHQAS GLGDVGEAFV DSLTSQVGGR SIGVYAVNYP ASDDYRASAS
30 91  NGSDDASAHI QRTVASCPNT RIVLGGYSQG ATVIDLSTSA MPPAVADHVA

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141 AVALFGEPSS GFSSMLWGGG SLPTIGPLYS SKTINLCAPD DPICTGGGNI
 191 MAHVSIVQSG MTSQAATFAA NRLDHAG

CFP22 (SEQ ID NO: 12):

1 MADCDSVTNS PLATATATLH TNRGDIKIAL FGNHAPKTVA NFGVLAQGTK
 5 51 DYSTQNASGG PSGPFYDGAV FHRVIQGFMI QGGDPTGTGR GGPYKFADE
 101 FHPELQFDKP YLLAMANAGP GTNGSQFFIT VGKTPHLNRR HTIFGEVIDA
 151 ESQRVVEAIS KTATDGND RP TDPVVIESIT IS

CFP25 (SEQ ID NO: 14):

1 MGAAAAMLAA VLLLTPTITVP AGYPGAVAPA TAACPDAEVV FARGRFEP
 10 51 IGTVGNAFVS ALRSKVNKNV GVIYAVKYPAD NQIDVGANDM SAHIQSMANS
 101 CPNTRLVPGG YSLGAAVTDV VLAVPTQMWG FTNPLPPGSD EHIAAVALFG
 151 NGSQWGPIT NFSPAYNDRT IELCHGDDPV CHPADPNTWE ANWPQHLAGA
 201 YVSSGMVNQA ADFVAGKLQ

CFP29 (SEQ ID NO: 16):

15 1 MNLYRDLAP VTEAAWAEIE LEAARTFKRH IAGRRVVDVS DPGGPVTA
 51 STGRLIDVKA PTNGVIAHLR ASKPLVRLRV PFTLSRNEID DVERGSKDSD
 101 WEPVKEAAKK LAFVEDRTIF EGYSAASIEG IRSASSNPAL TLPEDPREIP
 151 DVISQALSEL RLAGVDGPYS VLLSADVYTK VSETSDHGYP IREHLNRLVD
 201 GDIIWAPAI D GAFVLTTTRGG DFDLQLGTDV AIGYASHDTD TVRLYLQETL
 20 251 TFLCYTAEAS VALSH

For all six proteins the molecular weights predicted from the sequences are in agreement with the molecular weights observed on SDS-PAGE.

25 Cloning of the genes encoding CFP17, CFP20, CFP21, CFP22 and CFP25.

The genes encoding CFP17, CFP20, CFP21, CFP22 and CFP25 were all cloned into the expression vector pMCT6, by PCR amplification with gene specific primers, for recombinant expression in *E. coli* of the proteins.

PCR reactions contained 10 ng of *M. tuberculosis* chromosomal DNA in 1x low salt Taq+ buffer from Stratagene supplemented with 250 mM of each of the four nucleotides (Boehringer Mannheim), 0,5 mg/ml BSA (IgG technology), 1% DMSO (Merck), 5 pmoles of each primer and 0.5 unit Taq+ DNA polymerase (Stratagene) in 10 µl reaction volume. Reactions were initially heated to 94°C for 25 sec. and run for 30 cycles according to the following program; 94°C for 10 sec., 55°C for 10 sec. and 72°C for 90 sec, using thermocycler equipment from Idaho Technology.

The DNA fragments were subsequently run on 1% agarose gels, the bands were excised and purified by Spin-X spin columns (Costar) and cloned into pBluescript SK II+ - T vector (Stratagene). Plasmid DNA was thereafter prepared from clones harbouring the desired fragments, digested with suitable restriction enzymes and subcloned into the expression vector pMCT6 in frame with 8 histidine residues which are added to the N-terminal of the expressed proteins. The resulting clones were hereafter sequenced by use of the dideoxy chain termination method adapted for supercoiled DNA using the Sequenase DNA sequencing kit version 1.0 (United States Biochemical Corp., USA) and by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems) according to the instructions provided. Both strands of the DNA were sequenced.

For cloning of the individual antigens, the following gene specific primers were used:

CFP17: Primers used for cloning of cfp17:

OPBR-51:	ACAGATCTGTGACGGACATGAACCCG	(SEQ ID NO: 117)
OPBR-52:	TTTTCCATGGTCACGGGCCCCCGGTACT	(SEQ ID NO: 118)

OPBR-51 and OPBR-52 create BglII and NcoI sites, respectively, used for the cloning in pMCT6.

CFP20: Primers used for cloning of cfp20:

OPBR-53: ACAGATCTGTGCCCATGGCACAGATA (SEQ ID NO: 119)
 OPBR-54: TTTAAGCTTCTAGGCGCCAGCGCGGC (SEQ ID NO: 120)

OPBR-53 and OPBR-54 create BglII and HindIII sites, respectively, used for the cloning in pMCT6.

CFP21: Primers used for cloning of cfp21:

OPBR-55: ACAGATCTGCGCATGCGGATCCGTGT (SEQ ID NO: 121)
 OPBR-56: TTTTCCATGGTCATCCGGCGTGATCGAG (SEQ ID NO: 122)

OPBR-55 and OPBR-56 create BglII and NcoI sites, respectively, used for the cloning in pMCT6.

CFP22: Primers used for cloning of cfp22:

OPBR-57: ACAGATCTGTAATGGCAGACTGTGAT (SEQ ID NO: 123)
 OPBR-58: TTTTCCATGGTCAGGAGATGGTGATCGA (SEQ ID NO: 124)

OPBR-57 and OPBR-58 create BglII and NcoI sites, respectively, used for the cloning in pMCT6.

CFP25: Primers used for cloning of cfp25:

OPBR-59: ACAGATCTGCCGGCTACCCCGGTGCC (SEQ ID NO: 125)
 OPBR-60: TTTTCCATGGCTATTGCAGCTTTCCGGC (SEQ ID NO: 126)

OPBR-59 and OPBR-60 create BglII and NcoI sites, respectively, used for the cloning in pMCT6.

Expression/purification of recombinant CFP17, CFP20, CFP21, CFP22 and CFP25 proteins.

Expression and metal affinity purification of recombinant proteins was undertaken essentially as described by the manufacturers. For each protein, 1 l LB-media containing 100

μ g/ml ampicillin, was inoculated with 10 ml of an overnight culture of XL1-Blue cells harbouring recombinant pMCT6 plasmids. Cultures were shaken at 37 °C until they reached a density of $OD_{600} = 0.4 - 0.6$. IPTG was hereafter added to a
5 final concentration of 1 mM and the cultures were further incubated 4 - 16 hours. Cells were harvested, resuspended in 1X sonication buffer + 8 M urea and sonicated 5 X 30 sec. with 30 sec. pausing between the pulses.
After centrifugation, the lysate was applied to a column
10 containing 25 ml of resuspended Talon resin (Clontech, Palo Alto, USA). The column was washed and eluted as described by the manufacturers.

After elution, all fractions (1.5 ml each) were subjected to analysis by SDS-PAGE using the Mighty Small (Hoefer Scientific Instruments, USA) system and the protein concentrations
15 were estimated at 280 nm. Fractions containing recombinant protein were pooled and dialysed against 3 M urea in 10 mM Tris-HCl, pH 8.5. The dialysed protein was further purified by FPLC (Pharmacia, Sweden) using a 6 ml Resource-Q column,
20 eluted with a linear 0-1 M gradient of NaCl. Fractions were analyzed by SDS-PAGE and protein concentrations were estimated at OD_{280} . Fractions containing protein were pooled and dialysed against 25 mM Hepes buffer, pH 8.5.

Finally the protein concentration and the LPS content were
25 determined by the BCA (Pierce, Holland) and LAL (Endosafe, Charleston, USA) tests, respectively.

EXAMPLE 3A

Identification of CFP7A, CFP8A, CFP8B, CFP16, CFP19, CFP19B, CFP22A, CFP23A, CFP23B, CFP25A, CFP27, CFP30A, CWP32 and CFP50.

5 Identification of CFP16 and CFP19B.

ST-CF was precipitated with ammonium sulphate at 80% saturation. The precipitated proteins were removed by centrifugation and after resuspension washed with 8 M urea. CHAPS and glycerol were added to a final concentration of 0.5
10 % (w/v) and 5 % (v/v) respectively and the protein solution was applied to a Rotofor isoelectrical Cell (BioRad). The Rotofor Cell had been equilibrated with a 8M urea buffer containing 0.5 % (w/v) CHAPS, 5% (v/v) glycerol, 3% (v/v) Biolyt 3/5 and 1% (v/v) Biolyt 4/6 (BioRad). Isoelectric
15 focusing was performed in a pH gradient from 3-6. The fractions were analyzed on silver-stained 10-20% SDS-PAGE. Fractions with similar band patterns were pooled and washed three times with PBS on a Centriprep concentrator (Amicon) with a 3 kDa cut off membrane to a final volume of 1-3 ml. An equal
20 volume of SDS containing sample buffer was added and the protein solution boiled for 5 min before further separation on a Prep Cell (BioRad) in a matrix of 16% polyacrylamide under an electrical gradient. Fractions containing well separated bands in SDS-PAGE were selected for N-terminal
25 sequencing after transfer to PVDF membrane.

Isolation of CFP8A, CFP8B, CFP19, CFP23A, and CFP23B.

ST-CF was precipitated with ammonium sulphate at 80% saturation and redissolved in PBS, pH 7.4, and dialysed 3 times against 25mM Piperazin-HCl, pH 5.5, and subjected to chromatofocusing on a matrix of PBE 94 (Pharmacia) in a column
30 connected to an FPLC system (Pharmacia). The column was equilibrated with 25 mM Piperazin-HCl, pH 5.5, and the elution was performed with 10% PB74-HCl, pH 4.0 (Pharmacia).

Fractions with similar band patterns were pooled and washed three times with PBS on a Centriprep concentrator (Amicon) with a 3 kDa cut off membrane to a final volume of 1-3 ml and separated on a Prepcell as described above.

5 Identification of CFP22A

ST-CF was concentrated approximately 10 fold by ultrafiltration and proteins were precipitated at 80 % saturation, redissolved in PBS, pH 7.4, and dialysed 3 times against PBS, pH 7.4. 5.1 ml of the dialysed ST-CF was treated
10 with RNase (0.2 mg/ml, QUIAGEN) and DNase (0.2 mg/ml, Boehringer Mannheim) for 6 h and placed on top of 6.4 ml of 48 % (w/v) sucrose in PBS, pH 7.4, in Sorvall tubes (Ultracrimp 03987, DuPont Medical Products) and ultracentrifuged for 20 h at $257,300 \times g_{\max}$, 10°C. The pellet was redissolved in 200 μ l
15 of 25 mM Tris-192 mM glycine, 0.1 % SDS, pH 8.3.

Identification of CFP7A, CFP25A, CFP27, CFP30A and CFP50

For CFP27, CFP30A and CFP50 ST-CF was concentrated approximately 10 fold by ultrafiltration and ammonium sulphate precipitation in the 45 to 55 % saturation range was per-
20 formed. Proteins were redissolved in 50 mM sodium phosphate, 1.5 M ammonium sulphate, pH 8.5, and subjected to thiophilic adsorption chromatography on an Affi-T gel column (Kem-En-Tec). Proteins were eluted by a 1.5 to 0 M decreasing gradient of ammonium sulphate. Fractions with similar band
25 patterns in SDS-PAGE were pooled and anion exchange chromatography was performed on a Mono Q HR 5/5 column connected to an FPLC system (Pharmacia). The column was equilibrated with 10 mM Tris-HCl, pH 8.5, and the elution was performed with a gradient of NaCl from 0 to 1 M. Fractions containing well
30 separated bands in SDS-PAGE were selected.

CFP7A and CFP25A were obtained as described above except for the following modification: ST-CF was concentrated approximately 10 fold by ultrafiltration and proteins were precipi-

tated at 80 % saturation, redissolved in PBS, pH 7.4, and dialysed 3 times against PBS, pH 7.4. Ammonium sulphate was added to a concentration of 1.5 M, and ST-CF proteins were loaded on an Affi T-gel column. Elution from the Affi T-gel column and anion exchange were performed as described above.

Isolation of CWP32

Heat treated H37Rv was subfractionated into subcellular fractions as described in Sørensen et al 1995. The Cell wall fraction was resuspended in 8 M urea, 0.2 % (w/v) N-octyl β -D-glucopyranoside (Sigma) and 5 % (v/v) glycerol and the protein solution was applied to a Rotofor isoelectrical Cell (BioRad) which was equilibrated with the same buffer. Isoelectric focusing was performed in a pH gradient from 3-6. The fractions were analyzed by SDS-PAGE and fractions containing well separated bands were pooled and subjected to N-terminal sequencing after transfer to PVDF membrane.

N-terminal sequencing

Fractions containing CFP7A, CFP8A, CFP8B, CFP16, CFP19, CFP19B, CFP22A, CFP23A, CFP23B, CFP27, CFP30A, CWP32, and CFP50A were blotted to PVDF membrane after Tricine SDS-PAGE (Ploug et al, 1989). The relevant bands were excised and subjected to N-terminal amino acid sequence analysis on a Procise 494 sequencer (Applied Biosystems). The fraction containing CFP25A was blotted to PVDF membrane after 2-DE PAGE (isoelectric focusing in the first dimension and Tricin SDS-PAGE in the second dimension). The relevant spot was excised and sequenced as described above.

The following N-terminal sequences were obtained:

CFP7A:	AEDVRAEIVA SVLEVVVNEG DQIDKGDVVV LLESMYMEIP	
	VLAEAAGTVS	(SEQ ID NO: 81)
CFP8A:	DPVDDAFIAKLNTAG	(SEQ ID NO: 73)
CFP8B:	DPVDAIINLDNYGX	(SEQ ID NO: 74)

	CFP16:	AKLSTDELLDAFKEM	(SEQ ID NO: 79)
	CFP19:	TTSPDPYAALPKLPS	(SEQ ID NO: 82)
	CFP19B:	DPAXAPDVPTAAQLT	(SEQ ID NO: 80)
	CFP22A:	TEYEGPKTKF HALMQ	(SEQ ID NO: 83)
5	CFP23A:	VIQ/AGMVT/GHIHXVAG	(SEQ ID NO: 76)
	CFP23B:	AEMKXFKNAIVQEID	(SEQ ID NO: 75)
	CFP25A:	AIEVSVLRVF TDS DG	(SEQ ID NO: 78)
	CWP32:	TNIVVLIKQVPDTWS	(SEQ ID NO: 77)
	CFP27:	TTIVALKYPG GVVMA	(SEQ ID NO: 84)
10	CFP30A:	SFPYFISPEX AMRE	(SEQ ID NO: 85)
	CFP50:	THYDVVVLGA GPGGY	(SEQ ID NO: 86)

N-terminal homology searching in the Sanger database and identification of the corresponding genes.

The N-terminal amino acid sequence from each of the proteins was used for a homology search using the blast program of the Sanger *Mycobacterium tuberculosis* database:

<http://www.sanger.ac.uk/projects/m-tuberculosis/TB-blast-server>.

For CFP23B, CFP23A, and CFP19B no similarities were found in the Sanger database. This could be due to the fact that only approximately 70% of the *M. tuberculosis* genome had been sequenced when the searches were performed. The genes encoding these proteins could be contained in the remaining 30% of the genome for which no sequence data is yet available.

For CFP7A, CFP8A, CFP8B, CFP16, CFP19, CFP19B, CFP22A, CFP25A, CFP27, CFP30A, CWP32, and CFP50, the following information was obtained:

CFP7A: Of the 50 determined amino acids in CFP7A a 98% identical sequence was found in cosmid csCY07D1 (contig 256):
Score = 226 (100.4 bits), Expect = 1.4e-24, P = 1.4e-24
Identities = 49/50 (98%), Positives = 49/50 (98%), Frame = -1

Query: 1 AEDVRAEIVASVLEVVVNEGDQIDKGDVVVLLESMYMEIPVLAEAAGTVS 50
AEDVRAEIVASVLEVVVNEGDQIDKGDVVVLLESM MEIPVLAEAAGTVS
Sbjct: 257679 AEDVRAEIVASVLEVVVNEGDQIDKGDVVVLLESMKMEIPVLAEAAGTVS 257530

(SEQ ID NOs: 127, 128, and 129)

- 5 The identity is found within an open reading frame of 71 amino acids length corresponding to a theoretical MW of CFP7A of 7305.9 Da and a pI of 3.762. The observed molecular weight in an SDS-PAGE gel is 7 kDa.

- CFP8A: A sequence 80% identical to the 15 N-terminal amino acids was found on contig TB_1884. The N-terminally determined sequence from the protein purified from culture filtrate starts at amino acid 32. This gives a length of the mature protein of 98 amino acids corresponding to a theoretical MW of 9700 Da and a pI of 3.72 This is in good agreement with the observed MW on SDS-PAGE at approximately 8 kDa. The full length protein has a theoretical MW of 12989 Da and a pI of 4.38.

- CFP8B: A sequence 71% identical to the 14 N-terminal amino acids was found on contig TB_653. However, careful re-evaluation of the original N-terminal sequence data confirmed the identification of the protein. The N-terminally determined sequence from the protein purified from culture filtrate starts at amino acid 29. This gives a length of the mature protein of 82 amino acids corresponding to a theoretical MW of 8337 Da and a pI of 4.23. This is in good agreement with the observed MW on SDS-PAGE at approximately 8 kDa. Analysis of the amino acid sequence predicts the presence of a signal peptide which has been cleaved of the mature protein found in culture filtrate.

- 30 CFP16: The 15 aa N-terminal sequence was found to be 100% identical to a sequence found on cosmid MTCY20H1.

The identity is found within an open reading frame of 130 amino acids length corresponding to a theoretical MW of CFP16

of 13440.4 Da and a pI of 4.59. The observed molecular weight in an SDS-PAGE gel is 16 kDa.

CFP19: The 15 aa N-terminal sequence was found to be 100% identical to a sequence found on cosmid MTCY270.

- 5 The identity is found within an open reading frame of 176 amino acids length corresponding to a theoretical MW of CFP19 of 18633.9 Da and a pI of 5.41. The observed molecular weight in an SDS-PAGE gel is 19 kDa.

- CFP22A: The 15 aa N-terminal sequence was found to be 100% identical to a sequence found on cosmid MTCY1A6.

The identity is found within an open reading frame of 181 amino acids length corresponding to a theoretical MW of CFP22A of 20441.9 Da and a pI of 4.73. The observed molecular weight in an SDS-PAGE gel is 22 kDa.

- 15 CFP25A: The 15 aa N-terminal sequence was found to be 100% identical to a sequence found on contig 255.

The identity is found within an open reading frame of 228 amino acids length corresponding to a theoretical MW of CFP25A of 24574.3 Da and a pI of 4.95. The observed molecular weight in an SDS-PAGE gel is 25 kDa.

CFP27: The 15 aa N-terminal sequence was found to be 100% identical to a sequence found on cosmid MTCY261.

- 25 The identity is found within an open reading frame of 291 amino acids length. The N-terminally determined sequence from the protein purified from culture filtrate starts at amino acid 58. This gives a length of the mature protein of 233 amino acids, which corresponds to a theoretical molecular weight at 24422.4 Da, and a theoretical pI at 4.64. The observed weight in an SDS-PAGE gel is 27 kDa.

CFP30A: Of the 13 determined amino acids in CFP30A, a 100% identical sequence was found on cosmid MTCY261.

The identity is found within an open reading frame of 248 amino acids length corresponding to a theoretical MW of
5 CFP30A of 26881.0 Da and a pI of 5.41. The observed molecular weight in an SDS-PAGE gel is 30 kDa.

CWP32: The 15 amino acid N-terminal sequence was found to be 100% identical to a sequence found on contig 281. The identity was found within an open reading frame of 266 amino acids
10 length, corresponding to a theoretical MW of CWP32 of 28083 Da and a pI of 4.563. The observed molecular weight in an SDS-PAGE gel is 32 kDa.

CFP50: The 15 aa N-terminal sequence was found to be 100% identical to a sequence found in MTVO38.06. The identity is
15 found within an open reading frame of 464 amino acids length corresponding to a theoretical MW of CFP50 of 49244 Da and a pI of 5.66. The observed molecular weight in an SDS-PAGE gel is 50 kDa.

Use of homology searching in the EMBL database for identification of CFP19A and CFP23.
20

Homology searching in the EMBL database (using the GCG package of the Biobase, Århus-DK) with the amino acid sequences of two earlier identified highly immunoreactive ST-CF proteins, using the TFASTA algorithm, revealed that these proteins
25 (CFP21 and CFP25, EXAMPLE 3) belong to a family of fungal cutinase homologs. Among the most homologous sequences were also two *Mycobacterium tuberculosis* sequences found on cosmid MTCY13E12. The first, MTCY13E12.04 has 46% and 50% identity to CFP25 and CFP21 respectively. The second,
30 MTCY13E12.05, has also 46% and 50% identity to CFP25 and CFP21. The two proteins share 62.5% aa identity in a 184 residues overlap. On the basis of the high homology to the strong T-cell antigens CFP21 and CFP25, respectively, it is

believed that CFP19A and CFP23 are possible new T-cell antigens.

The first reading frame encodes a 254 amino acid protein of which the first 26 aa constitute a putative leader peptide
5 that strongly indicates an extracellular location of the protein. The mature protein is thus 228 aa in length corresponding to a theoretical MW of 23149.0 Da and a Pi of 5.80. The protein is named CFP23.

The second reading frame encodes an 231 aa protein of which
10 the first 44 aa constitute a putative leader peptide that strongly indicates an extracellular location of the protein. The mature protein is thus 187 aa in length corresponding to a theoretical MW of 19020.3 Da and a Pi of 7.03. The protein is named CFP19A.

15 The presence of putative leader peptides in both proteins (and thereby their presence in the ST-CF) is confirmed by theoretical sequence analysis using the signalP program at the Expasy molecular Biology server

(<http://expasy.hcuge.ch/www/tools.html>).

20 Searching for homologies to CFP7A, CFP16, CFP19, CFP19A, CFP19B, CFP22A, CFP23, CFP25A, CFP27, CFP30A, CWP32 and CFP50 in the EMBL database.

The amino acid sequences derived from the translated genes of the individual antigens were used for homology searching in
25 the EMBL and Genbank databases using the TFASTA algorithm, in order to find homologous proteins and to address eventual functional roles of the antigens.

CFP7A: CFP7A has 44% identity and 70% similarity to hypothetical *Methanococcus jannaschii* protein (*M. jannaschii* from
30 base 1162199-1175341), as well as 43% and 38% identity and 68 and 64% similarity to the C-terminal part of *B. stearothermo-*

philus pyruvate carboxylase and *Streptococcus mutans* biotin carboxyl carrier protein.

CFP7A contains a consensus sequence EAMKM for a biotin binding site motif which in this case was slightly modified
5 (ESMKM in amino acid residues 34 to 38). By incubation with alkaline phosphatase conjugated streptavidin after SDS-PAGE and transfer to nitrocellulose it was demonstrated that native CFP7A was biotinylated.

10 CFP16: RplL gene, 130 aa. Identical to the *M. bovis* 50S ribosomal protein L7/L12 (acc. No P37381).

CFP19: CFP19 has 47% identity and 55% similarity to *E.coli* pectinesterase homolog (ybhC gene) in a 150 aa overlap.

CFP19A: CFP19A has between 38% and 45% identity to several cutinases from different fungal sp.

15 In addition CFP19A has 46% identity and 61% similarity to CFP25 as well as 50% identity and 64% similarity to CFP21 (both proteins are earlier isolated from the ST-CF).

CFP19B: No apparent homology

CFP22A: No apparent homology

20 CFP23: CFP23 has between 38% and 46% identity to several cutinases from different fungal sp.

In addition CFP23 has 46% identity and 61% similarity to CFP25 as well as 50% identity and 63% similarity to CFP21 (both proteins are earlier isolated from the ST-CF).

25 CFP25A: CFP25A has 95% identity in a 241 aa overlap to a putative *M. tuberculosis* thymidylate synthase (450 aa accession No p28176).

CFP27: CFP27 has 81% identity to a hypothetical *M. leprae* protein and 64% identity and 78% similarity to *Rhodococcus* sp. proteasome beta-type subunit 2 (prcB(2) gene).

5 CFP30A: CFP30A has 67% identity to *Rhodococcus* proteasome alfa-type 1 subunit.

CWP32: The CWP32 N-terminal sequence is 100% identical to the *Mycobacterium leprae* sequence MLCB637.03.

10 CFP50: The CFP50 N-terminal sequence is 100% identical to a putative lipamide dehydrogenase from *M. leprae* (Accession 415183)

Cloning of the genes encoding CFP7A, CFP8A, CFP8B, CFP16, CFP19, CFP19A, CFP22A, CFP23, CFP25A, CFP27, CFP30A, CWP32, and CFP50.

15 The genes encoding CFP7A, CFP8A, CFP8B, CFP16, CFP19, CFP19A, CFP22A, CFP23, CFP25A, CFP27, CFP30A, CWP32 and CFP50 were all cloned into the expression vector pMCT6, by PCR amplification with gene specific primers, for recombinant expression in *E. coli* of the proteins.

20 PCR reactions contained 10 ng of *M. tuberculosis* chromosomal DNA in 1X low salt Taq+ buffer from Stratagene supplemented with 250 mM of each of the four nucleotides (Boehringer Mannheim), 0,5 mg/ml BSA (IgG technology), 1% DMSO (Merck), 5 pmoles of each primer and 0.5 unit Taq+ DNA polymerase (Stratagene) in 10 ml reaction volume. Reactions were initially
25 heated to 94°C for 25 sec. and run for 30 cycles of the program; 94°C for 10 sec., 55°C for 10 sec. and 72°C for 90 sec, using thermocycler equipment from Idaho Technology.

30 The DNA fragments were subsequently run on 1% agarose gels, the bands were excised and purified by Spin-X spin columns (Costar) and cloned into pBluescript SK II+ - T vector (Stratagene). Plasmid DNA was hereafter prepared from clones

harbouring the desired fragments, digested with suitable restriction enzymes and subcloned into the expression vector pMCT6 in frame with 8 histidines which are added to the N-terminal of the expressed proteins. The resulting clones were hereafter sequenced by use of the dideoxy chain termination method adapted for supercoiled DNA using the Sequenase DNA sequencing kit version 1.0 (United States Biochemical Corp., USA) and by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems) according to the instructions provided. Both strands of the DNA were sequenced.

For cloning of the individual antigens, the following gene specific primers were used:

CFP7A: Primers used for cloning of *cfp7A*:

15 OPBR-79: AAGAGTAGATCTATGATGGCCGAGGATGTTTCGCG (SEQ ID NO: 95)
OPBR-80: CGGCGACGACGGATCCTACCGCGTCGG (SEQ ID NO: 96)

OPBR-79 and OPBR-80 create *Bgl*III and *Bam*HI sites, respectively, used for the cloning in pMCT6.

CFP8A: Primers used for cloning of *cfp8A*:

20 CFP8A-F: CTGAGATCTATGAACCTACGGCGCC (SEQ ID NO: 154)
CFP8A-R: CTCCCATGGTACCCTAGGACCCGGGCAGCCCCGGC (SEQ ID NO: 155)

CFP8A-F and CFP8A-R create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP8B: Primers used for cloning of *cfp8B*:

25 CFP8B-F: CTGAGATCTATGAGGCTGTCTGTTGACCGC (SEQ ID NO: 156)
CFP8B-R: CTCCCCGGGCTTAATAGTTGTTGCAGGAGC (SEQ ID NO: 157)

CFP8B-F and CFP8B-R create *Bgl*III and *Sma*I sites, respectively, used for the cloning in pMCT6.

CFP16: Primers used for cloning of *cfp16*:OPBR-104: CCGGGAGATCTATGGCAAAGCTCTCCA~~C~~CGACG (SEQ ID NOs: 111 and 130)OPBR-105: CGCTGGGCAGAGCTACTT~~G~~ACGGTGACGGTGG (SEQ ID NOs: 112 and 131)

OPBR-104 and OPBR-105 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP19: Primers used for cloning of *cfp19*:

OPBR-96: GAGGAAGATCTATGACAACTTCACCCGACCCG (SEQ ID NO: 107)

OPBR-97: CATGAAGCCATGGCCCGCAGGCTGCATG (SEQ ID NO: 108)

OPBR-96 and OPBR-97 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP19A: Primers used for cloning of *cfp19A*:

OPBR-88: CCCCCAGATCTGCACCACCGGCATCGGCGGGC (SEQ ID NO: 99)

OPBR-89: GCGGCGGATCCGTTGCTTAGCCGG (SEQ ID NO: 100)

OPBR-88 and OPBR-89 create *Bgl*III and *Bam*HI sites, respectively, used for the cloning in pMCT6.

CFP22A: Primers used for cloning of *cfp22A*:

OPBR-90: CCGGCTGAGATCTATGACAGAATACGAAGGGC (SEQ ID NO: 101)

OPBR-91: CCCC GCCAGGGA~~A~~CTAGAGGCGGC (SEQ ID NO: 102)

OPBR-90 and OPBR-91 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP23: Primers used for cloning of *cfp23*:

OPBR-86: CCTTGGGAGATCTTTGGACCCCGGTTGC (SEQ ID NO: 97)

OPBR-87: GACGAGATCTTATGGGCTTACTGAC (SEQ ID NO: 98)

OPBR-86 and OPBR-87 both create a *Bgl*III site used for the cloning in pMCT6.

CFP25A: Primers used for cloning of *cfp25A*:

OPBR-106: GGCCCAGATCTATGGCCATTGAGGTTTCGGTGTTCG (SEQ ID NO: 113)
OPBR-107: CGCCGTGTTGCATGGCAGCGCTGAGC (SEQ ID NO: 114)

5 OPBR-106 and OPBR-107 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP27: Primers used for cloning of *cfp27*:

OPBR-92: CTGCCGAGATCTACCACCATTGTGCGCTGAAATACCC (SEQ ID NO: 103)
OPBR-93: CGCCATGGCCTTACGCGCCAACCTCG (SEQ ID NO: 104)

10 OPBR-92 and OPBR-93 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP30A: Primers used for cloning of *cfp30A*:

OPBR-94: GCGCGAGATCTGTGAGTTTTCCGTATTTTCATC (SEQ ID NO: 105)
OPBR-95: CGCGTCGAGCCATGGTTAGGCGCAG (SEQ ID NO: 106)

15 OPBR-94 and OPBR-95 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CWP32: Primers used for cloning of *cwp32*:

CWP32-F: GCTTAGATCTATGATTTTCTGGGCAACCAGGTA (SEQ ID NO: 158)
CWP32-R: GCTTCCATGGGCGAGGCACAGGCGTGGGAA (SEQ ID NO: 159)

20 CWP32-F and CWP32-R create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

CFP50: Primers used for cloning of *cfp50*:

OPBR-100: GGCCGAGATCTGTGACCCACTATGACGTCGTCG (SEQ ID NO: 109)
OPBR-101: GGCGCCCATGGTCAGAAATTGATCATGTGGCCAA (SEQ ID NO: 110)

25 OPBR-100 and OPBR-101 create *Bgl*III and *Nco*I sites, respectively, used for the cloning in pMCT6.

Expression/purification of recombinant CFP7A, CFP8A, CFP8B, CFP16, CFP19, CFP19A, CFP22A, CFP23, CFP25A, CFP27, CFP30A, CWP32, and CFP50 proteins.

- Expression and metal affinity purification of recombinant proteins was undertaken essentially as described by the manufacturers. For each protein, 1 l LB-media containing 100 µg/ml ampicillin, was inoculated with 10 ml of an overnight culture of XL1-Blue cells harbouring recombinant pMCT6 plasmids. Cultures were shaken at 37°C until they reached a density of $OD_{600} = 0.4 - 0.6$. IPTG was hereafter added to a final concentration of 1 mM and the cultures were further incubated 4-16 hours. Cells were harvested, resuspended in 1X sonication buffer + 8 M urea and sonicated 5 X 30 sec. with 30 sec. pausing between the pulses.
- After centrifugation, the lysate was applied to a column containing 25 ml of resuspended Talon resin (Clontech, Palo Alto, USA). The column was washed and eluted as described by the manufacturers.
- After elution, all fractions (1.5 ml each) were subjected to analysis by SDS-PAGE using the Mighty Small (Hoefer Scientific Instruments, USA) system and the protein concentrations were estimated at 280 nm. Fractions containing recombinant protein were pooled and dialysed against 3 M urea in 10 mM Tris-HCl, pH 8.5. The dialysed protein was further purified by FPLC (Pharmacia, Sweden) using a 6 ml Resource-Q column, eluted with a linear 0-1 M gradient of NaCl. Fractions were analyzed by SDS-PAGE and protein concentrations were estimated at OD_{280} . Fractions containing protein were pooled and dialysed against 25 mM Hepes buffer, pH 8.5.
- Finally the protein concentration and the LPS content were determined by the BCA (Pierce, Holland) and LAL (Endosafe, Charleston, USA) tests, respectively.

EXAMPLE 3B

Identification of CFP7B, CFP10A, CFP11 and CFP30B.

Isolation of CFP7B

ST-CF was precipitated with ammonium sulphate at 80% saturation and redissolved in PBS, pH 7.4, and dialyzed 3 times
5 against 25 mM Piperazin-HCl, pH 5.5, and subjected to chromatofocusing on a matrix of PBE 94 (Pharmacia) in a column connected to an FPLC system (Pharmacia). The column was equilibrated with 25 mM Piperazin-HCl, pH 5.5, and the elution
10 was performed with 10% PB74-HCl, pH 4.0 (Pharmacia). Fractions with similar band patterns were pooled and washed three times with PBS on a Centriprep concentrator (Amicon) with a 3 kDa cut off membrane to a final volume of 1-3 ml. An equal volume of SDS containing sample buffer was added and
15 the protein solution boiled for 5 min before further separation on a MultiEluter (BioRad) in a matrix of 10-20 % polyacrylamid (Andersen, P. & Heron, I., 1993). The fraction containing a well separated band below 10 kDa was selected for N-terminal sequencing after transfer to a PVDF membrane.

20 Isolation of CFP11

ST-CF was precipitated with ammonium sulphate at 80% saturation. The precipitated proteins were removed by centrifugation and after resuspension washed with 8 M urea. CHAPS and glycerol were added to a final concentration of 0.5 % (w/v)
25 and 5% (v/v) respectively and the protein solution was applied to a Rotofor isoelectrical Cell (BioRad). The Rotofor Cell had been equilibrated with an 8M urea buffer containing 0.5 % (w/v) CHAPS, 5% (v/v) glycerol, 3% (v/v) Biolyt 3/5 and 1% (v/v) Biolyt 4/6 (BioRad). Isoelectric focusing was per-
30 formed in a pH gradient from 3-6. The fractions were analyzed on silver-stained 10-20% SDS-PAGE. The fractions in the pH gradient 5.5 to 6 were pooled and washed three times with PBS on a Centriprep concentrator (Amicon) with a 3 kDa cut off

membrane to a final volume of 1 ml. 300 mg of the protein preparation was separated on a 10-20% Tricine SDS-PAGE (Ploug et al 1989) and transferred to a PVDF membrane and Coomassie stained. The lowest band occurring on the membrane was excised and submitted for N-terminal sequencing.

Isolation of CFP10A and CFP30B

ST-CF was concentrated approximately 10-fold by ultrafiltration and ammonium sulphate precipitation at 80 % saturation. Proteins were redissolved in 50 mM sodium phosphate, 1.5 M ammonium sulphate, pH 8.5, and subjected to thiophilic adsorption chromatography on an Affi-T gel column (Kem-En-Tec). Proteins were eluted by a 1.5 to 0 M decreasing gradient of ammonium sulphate. Fractions with similar band patterns in SDS-PAGE were pooled and anion exchange chromatography was performed on a Mono Q HR 5/5 column connected to an FPLC system (Pharmacia). The column was equilibrated with 10 mM Tris-HCl, pH 8.5, and the elution was performed with a gradient of NaCl from 0 to 1 M. Fractions containing well separated bands in SDS-PAGE were selected.

Fractions containing CFP10A and CFP30B were blotted to PVDF membrane after 2-DE PAGE (Ploug et al, 1989). The relevant spots were excised and subjected to N-terminal amino acid sequence analysis.

N-terminal sequencing

N-terminal amino acid sequence analysis was performed on a Procise 494 sequencer (Applied Biosystems).

The following N-terminal sequences were obtained:

CFP7B:	PQGTVKWFNAEKGFG	(SEQ ID NO: 168)
CFP10A:	NVTVSIPTILRPXXX	(SEQ ID NO: 169)
CFP11:	TRFMTDPHAMRDMAG	(SEQ ID NO: 170)
CFP30B:	PKRSEYRQGTNPWVD	(SEQ ID NO: 171)

"X" denotes an amino acid which could not be determined by the sequencing method used.

N-terminal homology searching in the Sanger database and identification of the corresponding genes.

- 5 The N-terminal amino acid sequence from each of the proteins was used for a homology search using the blast program of the Sanger *Mycobacterium tuberculosis* genome database:

<http://www.sanger.ac.uk/projects/m-tuberculosis/TB-blast-server>.

- 10 For CFP11 a sequence 100% identical to 15 N-terminal amino acids was found on contig TB_1314. The identity/was found within an open reading frame of 98 amino acids/length corresponding to a theoretical MW of 10977 Da and a pI of 5.14.

- 15 Amino acid number one can also be an Ala (insted of a Thr) as this sequence was also obtained (results not shown), and a 100% identical sequence to this N-terminal is found on contig TB_671 and on locus MTCI364.09.

- 20 For CFP7B a sequence 100% identical to 15 N-terminal amino acids was found on contig TB_2044 and on locus MTY15C10.04 with EMBL accession number: z95436. The identity was found within an open reading frame of 67 amino acids length corresponding to a theoretical MW of 7240 Da and a pI of 5.18.

- 25 For CFP10A a sequence 100% identical to 12 N-terminal amino acids was found on contig TB_752 and on locus CY130.20 with EMBL accession number: Q10646 and Z73902. The identity was found within an open reading frame of 93 amino acids length corresponding to a theoretical MW of 9557 Da and a pI of 4.78.

- 30 For CFP30B a sequence 100% identical to 15 N-terminal amino acids was found on contig TB_335. The identity was found within an open reading frame of 261 amino acids length

corresponding to a theoretical MW of 27345 Da and a pI of 4.24.

The amino acid sequences of the purified antigens as picked from the Sanger database are shown in the following list.

5 CFP7B (SEQ ID NO: 147)

1 MPQGTWKWFN AEKGFGFIAP EDGSADVFBH YTEIQGTGFR TLEENQKVEF
51 EIGHSPKGPQ ATGVRSL

CFP10A (SEQ ID NO: 141)

1 MNVTVSIPTI LRPHTGGQKS VSASGDTLGA VISDLEANYS GISERLMDPS
10 51 SPGKLHRFVN IYVNDEDVRF SGGLATAIAD GDSVTILPAV AGG

CFP11 protein sequence (SEQ ID NO: 143)

1 MATRFMTDPH AMRDMAGRFE VHAQTVEDEA RRMWASAQNI SGAGWSGMAE
51 ATSLDTMAQM NQAFRNIVNM LHGVRDGLVR DANNYEQQEQ ASQQILSS

CFP30B (SEQ ID NO: 145)

15 1 MPKRSEYRQG TPNWVDLQTT DQSAKKFYT SLFGWGYDDN PVPGGGGVYS
51 MATLNGEAVA AIAPMPPGAP EGMPIIWNTY IAVDDVDVAVV DKVVPGGGQV
101 MMPAFDIGDA GRMSFITDPT GAAVGLWQAN RHIGATLVNE TGTLIWNELL
151 TDKPDLALAF YEAVVGLTHS SMEIAAGQNY RVLKAGDAEV GGCMEPPMPG
201 VPNHWHVYFA VDDADATAAK AAAAGGQVIA EPADIPSVGR FAVLSDPQGA
20 251 IFSVLKPAPQ Q

Cloning of the genes encoding CFP7B, CFP10A, CFP11, and CFP30B.

PCR reactions contained 10 ng of *M. tuberculosis* chromosomal DNA in 1X low salt Taq+ buffer from Stratagene supplemented
25 with 250 mM of each of the four nucleotides (Boehringer Mannheim), 0,5 mg/ml BSA (IgG technology), 1% DMSO (Merck), 5 pmoles of each primer and 0.5 unit Taq+ DNA polymerase (Stra-

tagene) in 10 ml reaction volume. Reactions were initially heated to 94°C for 25 sec. and run for 30 cycles of the program; 94°C for 10 sec., 55°C for 10 sec. and 72°C for 90 sec., using thermocycler equipment from Idaho Technology.

- 5 The DNA fragments were subsequently run on 1% agarose gels, the bands were excised and purified by Spin-X spin columns (Costar) and cloned into pBluscript SK II+ - T vector (Stratagene). Plasmid DNA was hereafter prepared from clones harbouring the desired fragments, digested with suitable
- 10 restriction enzymes and subcloned into the expression vector pMCT6 in frame with 8 histidines which are added to the N-terminal of the expressed proteins. The resulting clones were hereafter sequenced by use of the dideoxy chain termination method adapted for supercoiled DNA using the Sequenase DNA
- 15 sequencing kit version 1.0 (United States Biochemical Corp., USA) and by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems) according to the instructions provided. Both strands of the DNA were sequenced.
- 20 For cloning of the individual antigens, the following gene specific primers were used:

CFP7B: Primers used for cloning of *cfp7B*:

CFP7B-F:	CTGAGATCTAGAATGCCACAGGGAAGTGTG	(SEQ ID NO: 160)
CFP7B-R:	TCTCCCGGGGGTAACTCAGAGCGAGCGGAC	(SEQ ID NO: 161)

- 25 CFP7B-F and CFP7B-R create *Bgl*III and *Sma*I sites, respectively, used for the cloning in pMCT6.

CFP10A: Primers used for cloning of *cfp10A*:

CFP10A-F:	CTGAGATCTATGAACGTCACCGTATCC	(SEQ ID NO: 162)
CFP10A-R:	TCTCCCGGGGGCTCACCACCGGCCACG	(SEQ ID NO: 163)

- 30 CFP10A -F and CFP10A -R create *Bgl*III and *Sma*I sites, respectively, used for the cloning in pMCT6.

CFP11: Primers used for cloning of *cfp11*:

CFP11-F:	CTGAGATCTATGGCAACACGTTTTATGACG	(SEQ ID NO: 164)
CFP11-R:	CTCCCCGGGTTAGCTGCTGAGGATCTGCTH	(SEQ ID NO: 165)

CFP11-F and CFP11-R create *Bgl*III and *Sma*I sites, respectively, used for the cloning in pMCT6.

CFP30B: Primers used for cloning of *cfp30B*:

CFP30B-F:	CTGAAGATCTATGCCCAAGAGAAGCGAATAC	(SEQ ID NO: 166)
CFP30B -R:	CGGCAGCTGCTAGCATTCTCCGAATCTGCCG	(SEQ ID NO: 167)

CFP30B-F and CFP30B-R create *Bgl*III and *Pvu*II sites, respectively, used for the cloning in pMCT6.

Expression/purification of recombinant CFP7B, CFP10A, CFP11 and CFP30B protein.

Expression and metal affinity purification of recombinant protein was undertaken essentially as described by the manufacturers. 1 l LB-media containing 100 µg/ml ampicillin, was inoculated with 10 ml of an overnight culture of XL1-Blue cells harbouring recombinant pMCT6 plasmid. The culture was shaken at 37 °C until it reached a density of OD₆₀₀ = 0.5. IPTG was hereafter added to a final concentration of 1 mM and the culture was further incubated 4 hours. Cells were harvested, resuspended in 1X sonication buffer + 8 M urea and sonicated 5 X 30 sec. with 30 sec. pausing between the pulses.

After centrifugation, the lysate was applied to a column containing 25 ml of resuspended Talon resin (Clontech, Palo Alto, USA). The column was washed and eluted as described by the manufacturers.

After elution, all fractions (1.5 ml each) were subjected to analysis by SDS-PAGE using the Mighty Small (Hoefer Scientific Instruments, USA) system and the protein concentrations

were estimated at 280 nm. Fractions containing recombinant protein were pooled and dialysed against 3 M urea in 10 mM Tris-HCl, pH 8.5. The dialysed protein was further purified by FPLC (Pharmacia, Sweden) using a 6 ml Resource-Q column, eluted with a linear 0-1 M gradient of NaCl. Fractions were analysed by SDS-PAGE and protein concentrations were estimated at OD₂₈₀. Fractions containing protein were pooled and dialysed against 25 mM Hepes buffer, pH 8.5.

Finally the protein concentration and the LPS content was determined by the BCA (Pierce, Holland) and LAL (Endosafe, Charleston, USA) tests, respectively.

EXAMPLE 4

Cloning of the gene expressing CFP26 (MPT51)

Synthesis and design of probes

Oligonucleotide primers were synthesized automatically on a DNA synthesizer (Applied Biosystems, Forster City, Ca, ABI-391, PCR-mode) deblocked and purified by ethanol precipitation.

Three oligonucleotides were synthesized (TABLE 3) on the basis of the nucleotide sequence from *mpb51* described by Ohara et al. (1995). The oligonucleotides were engineered to include an *EcoRI* restriction enzyme site at the 5' end and at the 3' end by which a later subcloning was possible.

Additional four oligonucleotides were synthesized on the basis of the nucleotide sequence from MPT51 (Fig. 5 and SEQ ID NO: 41). The four combinations of the primers were used for the PCR studies.

DNA cloning and PCR technology

Standard procedures were used for the preparation and handling of DNA (Sambrook et al., 1989). The gene *mpt51* was cloned from *M. tuberculosis* H37Rv chromosomal DNA by the use of the polymerase chain reactions (PCR) technology as described previously (Oettinger and Andersen, 1994). The PCR product was cloned in the pBluescriptSK + (Stratagene).

Cloning of *mpt51*

- 10 The gene, the signal sequence and the Shine Delgarno region of MPT51 was cloned by use of the PCR technology as two fragments of 952 bp and 815 bp in pBluescript SK +, designated pT052 and pT053.

DNA Sequencing

- 15 The nucleotide sequence of the cloned 952 bp *M. tuberculosis* H37Rv PCR fragment, pT052, containing the Shine Dalgarno sequence, the signal peptide sequence and the structural gene of MPT51, and the nucleotide sequence of the cloned 815 bp PCR fragment containing the structural gene of MPT51, pT053, were determined by the dideoxy chain termination method adapted for supercoiled DNA by use of the Sequenase DNA sequencing kit version 1.0 (United States Biochemical Corp., Cleveland, OH) and by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems) according to the instructions provided. Both strands of the DNA were sequenced.

- 20 The nucleotide sequences of pT052 and pT053 and the deduced amino acid sequence are shown in Figure 5. The DNA sequence contained an open reading frame starting with a ATG codon at position 45 - 47 and ending with a termination codon (TAA) at position 942 - 944. The nucleotide sequence of the first 33 codons was expected to encode the signal sequence. On the basis of the known N-terminal amino acid sequence (Ala - Pro

- Tyr - Glu - Asn) of the purified MPT51 (Nagai et al., 1991) and the features of the signal peptide, it is presumed that the signal peptidase recognition sequence (Ala-X-Ala) (von Heijne, 1984) is located in front of the N-terminal region of the mature protein at position 144. Therefore, a structural gene encoding MPT51, *mpt51*, derived from *M. tuberculosis* H37Rv was found to be located at position 144 - 945 of the sequence shown in Fig. 5. The nucleotide sequence of *mpt51* differed with one nucleotide compared to the nucleotide sequence of MPB51 described by Ohara et al. (1995) (Fig. 5). In *mpt51* at position 780 was found a substitution of a guanine to an adenine. From the deduced amino acid sequence this change occurs at a first position of the codon giving a amino acid change from alanine to threonine. Thus it is concluded, that *mpt51* consists of 801 bp and that the deduced amino acid sequence contains 266 residues with a molecular weight of 27,842, and MPT51 show 99,8% identity to MPB51.

Subcloning of *mpt51*

An *EcoRI* site was engineered immediately 5' of the first codon of *mpt51* so that only the coding region of the gene encoding MPT51 would be expressed, and an *EcoRI* site was incorporated right after the stop codon at the 3' end.

DNA of the recombinant plasmid pTO53 was cleaved at the *EcoRI* sites. The 815 bp fragment was purified from an agarose gel and subcloned into the *EcoRI* site of the pMAL-cR1 expression vector (New England Biolabs), pTO54. Vector DNA containing the gene fusion was used to transform the *E. coli* XL1-Blue by the standard procedures for DNA manipulation.

The endpoints of the gene fusion were determined by the dideoxy chain termination method as described under section DNA sequencing. Both strands of the DNA were sequenced.

Preparation and purification of rMPT51

Recombinant antigen was prepared in accordance with instructions provided by New England Biolabs. Briefly, single colonies of *E. coli* harbouring the pT054 plasmid were inoculated into Luria-Bertani broth containing 50 µg/ml ampicillin and 12.5 µg/ml tetracycline and grown at 37°C to 2×10^8 cells/ml. Isopropyl-β-D-thiogalactoside (IPTG) was then added to a final concentration of 0.3 mM and growth was continued for further 2 hours. The pelleted bacteria were stored overnight at -20°C in new column buffer (20 mM Tris/HCl, pH 7.4, 200 mM NaCl, 1 mM EDTA, 1 mM dithiothreitol (DTT)) and thawed at 4°C followed by incubation with 1 mg/ml lysozyme on ice for 30 min and sonication (20 times for 10 sec with intervals of 20 sec). After centrifugation at 9,000 x g for 30 min at 4°C, the maltose binding protein -MPT51 fusion protein (MBP-rMPT51) was purified from the crude extract by affinity chromatography on amylose resin column. MBP-rMPT51 binds to amylose. After extensive washes of the column, the fusion protein was eluted with 10 mM maltose. Aliquots of the fractions were analyzed on 10% SDS-PAGE. Fractions containing the fusion protein of interest were pooled and was dialysed extensively against physiological saline.

Protein concentration was determined by the BCA method supplied by Pierce (Pierce Chemical Company, Rockford, IL).

TABLE 3.

Orientation and oligonucleotide ^a		Sequence of the <i>mpt51</i> oligonucleotides ^a . Sequences (5' → 3')	Position ^b (nucleotide)
5	Sense		
	MPT51-1	<u>CTCGAATTC</u> GCCGGGTGCACACAG (SEQ ID NO: 28)	6 - 21 (SEQ ID NO: 41)
	MPT51-3	<u>CTCGAATTC</u> GCCCCATACGAGAAC (SEQ ID NO: 29)	143 - 158 (SEQ ID NO: 41)
	MPT51-5	GTGTATCTGCTGGAC (SEQ ID NO: 30)	228 - 242 (SEQ ID NO: 41)
	MPT51-7	CCGACTGGCTGGCCG (SEQ ID NO: 31)	418 - 432 (SEQ ID NO: 41)
10	Antisense		
	MPT51-2	<u>GAGGAATTC</u> GCTTAGCGGATCGCA (SEQ ID NO: 32)	946 - 932 (SEQ ID NO: 41)
	MPT51-4	CCCACATTCCTGG (SEQ ID NO: 33)	642 - 628 (SEQ ID NO: 41)
	MPT51-6	GTCCAGCAGATACAC (SEQ ID NO: 34)	242 - 228 (SEQ ID NO: 41)

^a The oligonucleotides MPT51-1 and MPT51-2 were constructed from the MPB51 nucleotide sequence (Ohara et al., 1995). The other oligonucleotides constructions were based on the nucleotide sequence obtained from *mpt51* reported in this work. Nucleotides (nt) underlined are not contained in the nucleotide sequence of MPB/T51.

^b The positions referred to are of the non-underlined parts of the primers and correspond to the nucleotide sequence shown in SEQ ID NO: 41.

Cloning of *mpt51* in the expression vector pMST24.

A PCR fragment was produced from pT052 using the primer combination MPT51-F and MPT51-R (TABLE 4). A *Bam*HI site was engineered immediately 5' of the first codon of *mpt51* so that only the coding region of the gene encoding MPT51 would be expressed, and an *Nco*I site was incorporated right after the stop codon at the 3' end.

The PCR product was cleaved at the *Bam*HI and the *Nco*I site. The 811 bp fragment was purified from an agarose gel and subcloned into the *Bam*HI and the *Nco*I site of the pMST24 expression vector, pT086. Vector DNA containing the gene fusion was used to transform the *E. coli* XL1-Blue by the standard procedures for DNA manipulation.

The nucleotide sequence of complete gene fusion was determined by the dideoxy chain termination method as described under section DNA sequencing. Both strands of the DNA were sequenced.

Preparation and purification of rMPT51.

Recombinant antigen was prepared from single colonies of *E. coli* harbouring the pT086 plasmid inoculated into Luria-Bertani broth containing 50 µg/ml ampicillin and 12.5 µg/ml tetracycline and grown at 37°C to 2×10^8 cells/ml. Isopropyl-β-D-thiogalactoside (IPTG) was then added to a final concentration of 1 mM and growth was continued for further 2 hours. The pelleted bacteria were resuspended in BC 100/20 buffer (100 mM KCl, 20 mM Imidazole, 20 mM Tris/HCl, pH 7.9, 20 % glycerol). Cells were broken by sonication (20 times for 10 sec with intervals of 20 sec). After centrifugation at 9,000 x g for 30 min. at 4°C the insoluble matter was resuspended in BC 100/20 buffer with 8 M urea followed by sonication and centrifugation as above. The His tag-MPT51 fusion protein (His-rMPT51) was purified by affinity chromatography on Ni-NTA resin column (Qiagen, Hilden, Germany). His-rMPT51 binds to Ni-NTA. After extensive washes of the column, the fusion protein was eluted with BC 100/40 buffer (100 mM KCl, 40 mM Imidazole, 20 mM Tris/HCl, pH 7.9, 20 % glycerol) with 8 M urea and BC 1000/40 buffer (1000 mM KCl, 40 mM Imidazole, 20 mM Tris/HCl, pH 7.9, 20 % glycerol) with 8 M urea. His-rMPT51 was extensively dialysed against 10 mM Tris/HCl, pH 8.5, 3 M urea followed by purification using fast protein liquid chromatography (FPLC) (Pharmacia, Uppsala, Sweden), over an anion exchange column (Mono Q) using 10 mM Tris/HCl, pH 8.5, 3 M urea with a 0 - 1 M NaCl linear gradient. Fractions containing rMPT51 were pooled and subsequently dialysed extensively against 25 mM Hepes, pH 8.0 before use.

Protein concentration was determined by the BCA method supplied by Pierce (Pierce Chemical Company, Rockford, IL). The lipopolysaccharide (LPS) content was determined by the limulus amoebocyte lysate test (LAL) to be less than 0.004 ng/µg rMPT51, and this concentration had no influence on cellular activity.

TABLE 4. Sequence of the *mpt51* oligonucleotides.

Orientation and oligonucleotide		Sequences (5' → 3')	Position (nt)
Sense			
5	MPT51-F	<u>CTCGGATCCTGCCCCATACGAGAACCTG</u>	139 - 156
Antisense			
	MPT51-R	<u>CTCCCATGGTTAGCGGATCGCACCG</u>	939 - 924

EXAMPLE 4A

Cloning of the ESAT6-MPT59 and the MPT59-ESAT6 hybrids.

10 Background for ESAT-MPT59 and MPT59-ESAT6 fusion

Several studies have demonstrated that ESAT-6 is a an immunogen which is relatively difficult to adjuvate in order to obtain consistent results when immunizing therewith. To detect an *in vitro* recognition of ESAT-6 after immunization with the antigen is very difficult compared to the strong recognition of the antigen that has been found during the recall of memory immunity to *M. tuberculosis*. ESAT-6 has been found in ST-CF in a truncated version were amino acids 1-15 have been deleted. The deletion includes the main T-cell epitopes recognized by C57BL/6j mice (Brandt et al., 1996). This result indicates that ESAT-6 either is N-terminally processed or proteolytically degraded in STCF. In order to optimize ESAT-6 as an immunogen, a gene fusion between ESAT-6 and another major T cell antigen MPT59 has been constructed. Two different construct have been made: MPT59-ESAT-6 (SEQ ID NO: 172) and ESAT-6-MPT59 (SEQ ID NO: 173). In the first hybrid ESAT-6 is N-terminally protected by MPT59 and in the latter it is expected that the fusion of two dominant T-cell antigens can have a synergistic effect.

The genes encoding the ESAT6-MPT59 and the MPT59-ESAT6 hybrids were cloned into the expression vector pMCT6, by PCR amplification with gene specific primers, for recombinant expression in *E. coli* of the hybrid proteins.

5 Construction of the hybrid MPT59-ESAT6.

The cloning was carried out in three steps. First the genes encoding the two components of the hybrid, ESAT6 and MPT59, were PCR amplified using the following primer constructions:

ESAT6:

- 10 OPBR-4: GGCGCCGGCAAGCTTGCCATGACAGAGCAGCAGTGG (SEQ ID NO: 132)
OPBR-28: CGAACTCGCCGGATCCCGTGTTCGC (SEQ ID NO: 133)

OPBR-4 and OPBR-28 create HindIII and BamHI sites, respectively.

MPT59:

- 15 OPBR-48: GGCAACCGCGAGATCTTTCTCCCGCCGGGGC (SEQ ID NO: 134)
OPBR-3: GGCAAGCTTGCCGGCGCCTAACGAAC (SEQ ID NO: 135)

OPBR-48 and OPBR-3 create BglII and HindIII, respectively. Additionally OPBR-3 deletes the stop codon of MPT59.

- 20 PCR reactions contained 10 ng of *M. tuberculosis* chromosomal DNA in 1x low salt Taq+ buffer from Stratagene supplemented with 250 mM of each of the four nucleotides (Boehringer Mannheim), 0,5 mg/ml BSA (IgG technology), 1% DMSO (Merck), 5 pmoles of each primer and 0.5 unit Taq+ DNA polymerase (Stratagene) in 10 µl reaction volume. Reactions were initially
25 heated to 94°C for 25 sec. and run for 30 cycles of the program; 94°C for 10 sec., 55°C for 10 sec. and 72°C for 90 sec, using thermocycler equipment from Idaho Technology.

The DNA fragments were subsequently run on 1% agarose gels, the bands were excised and purified by Spin-X spin columns

- (Costar). The two PCR fragments were digested with *HinDIII* and ligated. A PCR amplification of the ligated PCR fragments encoding MPT59-ESAT6 was carried out using the primers OPBR-48 and OPBR-28. PCR reaction was initially heated to 94°C for 25 sec. and run for 30 cycles of the program; 94°C for 30 sec., 55°C for 30 sec. and 72°C for 90 sec. The resulting PCR fragment was digested with *BglII* and *BamHI* and cloned into the expression vector pMCT6 in frame with 8 histidines which are added to the N-terminal of the expressed protein hybrid.
- The resulting clones were hereafter sequenced by use of the dideoxy chain termination method adapted for supercoiled DNA using the Sequenase DNA sequencing kit version 1.0 (United States Biochemical Corp., USA) and by cycle sequencing using the Dye Terminator system in combination with an automated gel reader (model 373A; Applied Biosystems) according to the instructions provided. Both strands of the DNA were sequenced.

Construction of the hybrid ESAT6-MPT59.

- Construction of the hybrid ESAT6-MPT59 was carried out as described for the hybrid MPT59-ESAT6. The primers used for the construction and cloning were:

ESAT6:

OPBR-75: GGACCCAGATCTATGACAGAGCAGCAGTGG (SEQ ID NO: 136)
OPBR-76: CCGGCAGCCCCGGCCGGGAGAAAAGCTTTGCGAACATCCCAGTGACG (SEQ ID NO: 137)

- OPBR-75 and OPBR-76 create *BglII* and *HinDIII* sites, respectively. Additionally OPBR-76 deletes the stop codon of ESAT6.

MPT59:

OPBR-77: GTTCGCAAAGCTTTTCTCCCGGCCGGGGCTGCCGGTCGAGTACC (SEQ ID NO: 138)
OPBR-18: CCTTCGGTGGATCCCGTCAG (SEQ ID NO: 139)

- OPBR-77 and OPBR-18 create *HinDIII* and *BamHI* sites, respectively.

Expression/purification of MPT59-ESAT6 and ESAT6-MPT59 hybrid proteins.

Expression and metal affinity purification of recombinant proteins was undertaken essentially as described by the manufacturers. For each protein, 1 l LB-media containing 100 μ g/ml ampicillin, was inoculated with 10 ml of an overnight culture of XL1-Blue cells harbouring recombinant pMCT6 plasmids. Cultures were shaken at 37 °C until they reached a density of $OD_{600} = 0.4 - 0.6$. IPTG was hereafter added to a final concentration of 1 mM and the cultures were further incubated 4 - 16 hours. Cells were harvested, resuspended in 1X sonication buffer + 8 M urea and sonicated 5 X 30 sec. with 30 sec. pausing between the pulses.

After centrifugation, the lysate was applied to a column containing 25 ml of resuspended Talon resin (Clontech, Palo Alto, USA). The column was washed and eluted as described by the manufacturers.

After elution, all fractions (1.5 ml each) were subjected to analysis by SDS-PAGE using the Mighty Small (Hoefer Scientific Instruments, USA) system and the protein concentrations were estimated at 280 nm. Fractions containing recombinant protein were pooled and dialysed against 3 M urea in 10 mM Tris-HCl, pH 8.5. The dialysed protein was further purified by FPLC (Pharmacia, Sweden) using a 6 ml Resource-Q column, eluted with a linear 0-1 M gradient of NaCl. Fractions were analyzed by SDS-PAGE and protein concentrations were estimated at OD_{280} . Fractions containing protein were pooled and dialysed against 25 mM Hepes buffer, pH 8.5.

Finally the protein concentration and the LPS content were determined by the BCA (Pierce, Holland) and LAL (Endosafe, Charleston, USA) tests, respectively.

The biological activity of the MPT59-ESAT6 fusion protein is described in Example 6A.

EXAMPLE 5

Mapping of the purified antigens in a 2DE system.

In order to characterize the purified antigens they were mapped in a 2-dimensional electrophoresis (2DE) reference system. This consists of a silver stained gel containing ST-CF proteins separated by isoelectrical focusing followed by a separation according to size in a polyacrylamide gel electrophoresis. The 2DE was performed according to Hochstrasser et al. (1988). 85 μ g of ST-CF was applied to the isoelectrical focusing tubes where BioRad ampholytes BioLyt 4-6 (2 parts) and BioLyt 5-7 (3 parts) were included. The first dimension was performed in acrylamide/piperazin diacrylamide tube gels in the presence of urea, the detergent CHAPS and the reducing agent DTT at 400 V for 18 hours and 800 V for 2 hours. The second dimension 10-20% SDS-PAGE was performed at 100 V for 18 hours and silver stained. The identification of CFP7, CFP7A, CFP7B, CFP8A, CFP8B, CFP9, CFP11, CFP16, CFP17, CFP19, CFP20, CFP21, CFP22, CFP25, CFP27, CFP28, CFP29, CFP30A, CFP50, and MPT51 in the 2DE reference gel were done by comparing the spot pattern of the purified antigen with ST-CF with and without the purified antigen. By the assistance of an analytical 2DE software system (Phoretix International, UK) the spots have been identified in Fig. 6. The position of MPT51 and CFP29 were confirmed by a Western blot of the 2DE gel using the Mab's anti-CFP29 and HBT 4.

EXAMPLE 6

*Biological activity of the purified antigens.*IFN- γ induction in the mouse model of TB infection

The recognition of the purified antigens in the mouse model of memory immunity to TB (described in example 1) was investigated. The results shown in TABLE 5 are representative for three experiments.

A very high IFN- γ response was induced by two of the antigens CFP17 and CFP21 at almost the same high level as ST-CF.

TABLE 5

5 IFN- γ release from splenic memory effector cells from C57BL/6J mice isolated after reinfection with *M. tuberculosis* after stimulation with native antigens.

	Antigen ^a	IFN- γ (pg/ml) ^b
	ST-CF	12564
	CFP7	ND ^d
10	CFP9	ND
	CFP17	9251
	CFP20	2388
	CFP21	10732
	CFP22 + CFP25 ^c	5342
15	CFP26 (MPT51)	ND
	CFP28	2818
	CFP29	3700

The data is derived from a representative experiment out of three.

20 ^a ST-CF was tested in a concentration of 5 μ g/ml and the individual antigens in a concentration of 2 μ g/ml.

^b Four days after rechallenge a pool of cells from three mice were tested. The results are expressed as mean of duplicate values and the difference between duplicate cultures are < 15% of mean. The IFN- γ release of cultures incubated without antigen was 390 pg/ml.

25 ^c A pool of CFP22 and CFP25 was tested.

^d ND, not determined.

Skin test reaction in TB infected guinea pigs

The skin test activity of the purified proteins was tested in *M. tuberculosis* infected guinea pigs.

30 1 group of guinea pigs was infected via an ear vein with 1 x 10⁴ CFU of *M. tuberculosis* H37Rv in 0,2 ml PBS. After 4

weeks skin tests were performed and 24 hours after injection erythema diameter was measured.

As seen in TABLES 6 and 6a all of the antigens induced a significant Delayed Type Hypersensitivity (DTH) reaction.

5

TABLE 6

DTH erythema diameter in guinea pigs infected with 1×10^4 CFU of *M. tuberculosis*, after stimulation with native antigens.

	Antigen ^a	Skin reaction (mm) ^b
	Control	2.00
10	PPD ^c	15.40 (0.53)
	CFP7	ND ^e
	CFP9	ND
	CFP17	11.25 (0.84)
	CFP20	8.88 (0.13)
15	CFP21	12.44 (0.79)
	CFP22 + CFP25 ^d	9.19 (3.10)
	CFP26 (MPT51)	ND
	CFP28	2.90 (1.28)
	CFP29	6.63 (0.88)

20 The values presented are the mean of erythema diameter of four animals and the SEM's are indicated in the brackets. For PPD and CFP29 the values are mean of erythema diameter of ten animals.

^a The antigens were tested in a concentration of 0,1 µg except for CFP29 which was tested in a concentration of 0,8 µg.

25 ^b The skin reactions are measured in mm erythema 24 h after intradermal injection.

^c 10 TU of PPD was used.

^d A pool of CFP22 and CFP25 was tested.

^e ND, not determined.

30 Together these analyses indicate that most of the antigens identified were highly biologically active and recognized during TB infection in different animal models.

TABLE 6a

DTH erythema diameter of recombinant antigens in outbred guinea pigs infected with 1×10^4 CFU of *M. Tuberculosis*.

	Antigen ^a	Skin reaction (mm) ^b	
5	Control	2.9	(0.3)
	PPD ^c	14.5	(1.0)
	CFP 7a	13.6	(1.4)
	CFP 17	6.8	(1.9)
	CFP 20	6.4	(1.4)
10	CFP 21	5.3	(0.7)
	CFP 25	10.8	(0.8)
	CFP 29	7.4	(2.2)
	MPT 51	4.9	(1.1)

The values presented are the mean of erythema diameter of four animals and the SEM's are indicated in the brackets. For Control, PPD, and CFP 20 the values are mean of erythema diameter of eight animals.

^a The antigens were tested in a concentration of 1,0 µg.

^b The skin test reactions are measured in mm erythema 24 h after intradermal infection.

^c 10 TU of PPD was used.

Biological activity of the purified recombinant antigens.

Interferon-γ induction in the mouse model of TB infection.

Primary infections. 8 to 12 weeks old female C57BL/6j (H-2^b), CBA/J (H-2^k), DBA.2 (H-2^d) and A.SW (H-2^s) mice (Bomholtegaard, Ry) were given intravenous infections via the lateral tail vein with an inoculum of 5×10^4 *M. tuberculosis* suspended in PBS in a vol. of 0.1 ml. 14 days postinfection the animals were sacrificed and spleen cells were isolated and tested for the recognition of recombinant antigen.

As seen in TABLE 7 the recombinant antigens rCFP7A, rCFP17, rCFP21, rCFP25, and rCFP29 were all recognized in at least two strains of mice at a level comparable to ST-CF. rMPT51 and rCFP7 were only recognized in one or two strains respectively, at a level corresponding to no more than 1/3 of the

response detected after ST-CF stimulation. Neither of the antigens rCFP20 and rCFP22 were recognized by any of the four mouse strains.

Memory responses. 8-12 weeks old female C57BL/6j (H-2^b) mice (Bomholtegaard, Ry) were given intravenous infections via the lateral tail vein with an inoculum of 5×10^4 *M. tuberculosis* suspended in PBS in a vol. of 0.1 ml. After 1 month of infection the mice were treated with isoniazid (Merck and Co., Rahway, NJ) and rifabutin (Farmatalia Carlo Erba, Milano, Italy) in the drinking water, for two months. The mice were rested for 4-6 months before being used in experiments. For the study of the recall of memory immunity, animals were infected with an inoculum of 1×10^6 bacteria i.v. and sacrificed at day 4 postinfection. Spleen cells were isolated and tested for the recognition of recombinant antigen.

As seen from TABLE 8, IFN- γ release after stimulation with rCFP17, rCFP21 and rCFP25 was at the same level as seen from spleen cells stimulated with ST-CF. Stimulation with rCFP7, rCFP7A and rCFP29 all resulted in an IFN- γ no higher than 1/3 of the response seen with ST-CF. rCFP22 was not recognized by IFN- γ producing cells. None of the antigens stimulated IFN- γ release in naive mice. Additionally none of the antigens were toxic to the cell cultures.

TABLE 7. T cell responses in primary TB infection.

Name	c57BL/6J (H2 ^b)	DBA.2 (H2 ^d)	CBA/J (H2 ^k)	A.SW (H2 ^s)
rCFP7	+	+	-	-
rCFP7A	+++	+++	+++	+
5 rCFP17	+++	+	+++	+
rCFP20	-	-	-	-
rCFP21	+++	+++	+++	+
rCFP22	-	-	-	-
rCFP25	+++	++	+++	+
10 rCFP29	+++	+++	+++	++
rMPT51	+	-	-	-

Mouse IFN- γ release during recall of memory immunity to *M. tuberculosis*.

-: no response; +: 1/3 of ST-CF; ++: 2/3 of ST-CF; +++: level
15 of ST-CF.

TABLE 8. T cell responses in memory immune animals.

Name	Memory response
rCFP7	+
rCFP7A	++
20 rCFP17	+++
rCFP21	+++
rCFP22	-
rCFP29	+
rCFP25	+++
25 rMPT51	+

Mouse IFN- γ release 14 days after primary infection with *M. tuberculosis*.

-: no response; +: 1/3 of ST-CF; ++: 2/3 of ST-CF; +++: level
of ST-CF.

Interferon- γ induction in human TB patients and BCG vaccinated people.

Human donors: PBMC were obtained from healthy BCG vaccinated donors with no known exposure to patients with TB and from
5 patients with culture or microscopy proven infection with *Mycobacterium tuberculosis*. Blood samples were drawn from the TB patients 1-4 months after diagnosis.

Lymphocyte preparations and cell culture: PBMC were freshly isolated by gradient centrifugation of heparinized blood on
10 Lymphoprep (Nycomed, Oslo, Norway). The cells were resuspended in complete medium: RPMI 1640 (Gibco, Grand Island, N.Y.) supplemented with 40 μ g/ml streptomycin, 40 U/ml penicillin, and 0.04 mM/ml glutamine, (all from Gibco Laboratories, Paisley, Scotland) and 10% normal human ABO serum (NHS) from
15 the local blood bank. The number and the viability of the cells were determined by trypan blue staining. Cultures were established with $2,5 \times 10^5$ PBMC in 200 μ l in microtitre plates (Nunc, Roskilde, Denmark) and stimulated with no antigen, ST-CF, PPD (2.5 μ g/ml); rCFP7, rCFP7A, rCFP17,
20 rCFP20, rCFP21, rCFP22, rCFP25, rCFP26, rCFP29, in a final concentration of 5 μ g/ml. Phytohaemagglutinin, 1 μ g/ml (PHA, Difco laboratories, Detroit, MI. was used as a positive control. Supernatants for the detection of cytokines were harvested after 5 days of culture, pooled and stored at -80°C
25 until use.

Cytokine analysis: Interferon- γ (IFN- γ) was measured with a standard ELISA technique using a commercially available pair of mAb's from Endogen and used according to the instructions for use. Recombinant IFN- γ (Gibco laboratories) was used as
30 a standard. The detection level for the assay was 50 pg/ml. The variation between the duplicate wells did not exceed 10 % of the mean. Responses of 9 individual donors are shown in TABLE 9.

A seen in TABLE 9 high levels of IFN- γ release are obtained after stimulation with several of the recombinant antigens. rCFP7a and rCFP17 gives rise to responses comparable to STCF in almost all donors. rCFP7 seems to be most strongly recognized by BCG vaccinated healthy donors. rCFP21, rCFP25, rCFP26, and rCFP29 gives rise to a mixed picture with intermediate responses in each group, whereas low responses are obtained by rCFP20 and rCFP22.

TABLE 9. Mean values of results from the stimulation of human blood cells from 7 BCG vaccinated and 7 TB patients with recombinant antigens. SE values are given for each antigen. ST-CF and *M. avium* culture filtrate are shown for the comparison.

Controls, Healthy, BCG vaccinated, no known TB exposure

donor:	no ag	PHA	PPD	STCF	CFP7	CFP17	CFP7A	CFP20	CFP21	CFP22	CFP25	CFP26	CFP29
1	6	9564	6774	3966	7034	69	1799	58	152	73	182	946	86
2	48	12486	6603	8067	3146	10044	5267	29	6149	51	1937	526	2065
3	190	11929	10000	8299	8015	11563	8641	437	3194	669	2531	8076	6098
4	10	21029	4106	3537	1323	1939	5211	1	284	1	1344	20	125
5	1	18750	14209	13027	17725	8038	19002	1	3008	1	2103	974	8181

TB patients, 1-4 month after diagnosis

	no ag	PHA	PPD	STCF	CFP7	CFP17	CFP7A	CFP20	CFP21	CFP22	CFP25	CFP26	CFP29
6	9	8973	5096	6145	852	4250	4019	284	1131	48	2400	1078	4584
7	1	12413	6281	3393	168	6375	4505	11	4335	16	3082	1370	5115
8	4	11915	7671	7375	104	2753	3356	119	407	437	2069	712	5284
9	32	22130	16417	17213	8450	9783	16319	91	5957	67	10043	13313	9953

Example 6A

Four groups of 6-8 weeks old, female C57Bl/6J mice (Bomholte-gård, Denmark) were immunized subcutaneously at the base of the tail with vaccines of the following compositions:

- 5 Group 1: 10 μ g ESAT-6/DDA (250 μ g)
 Group 2: 10 μ g MPT59/DDA (250 μ g)
 Group 3: 10 μ g MPT59-ESAT-6 /DDA (250 μ g)
 Group 4: Adjuvant control group: DDA (250 μ g) in NaCl

10 The animals were injected with a volume of 0.2 ml. Two weeks after the first injection and 3 weeks after the second injection the mice were boosted a little further up the back. One week after the last immunization the mice were bled and the blood cells were isolated. The immune response induced was monitored by release of IFN- γ into the culture supernatants when stimulated in vitro with relevant antigens (see the
 15 following table).

Immunogen 10 μ g/dose	For restimulation ^{a)} : Ag in vitro			
	no antigen	ST-CF	ESAT-6	MPT59
20 ESAT-6	219 \pm 219	569 \pm 569	835 \pm 633	-
MPT59	0	802 \pm 182	-	5647 \pm 159
Hybrid: MPT59-ESAT-6	127 \pm 127	7453 \pm 581	15133 \pm 861	16363 \pm 1002

- a) Blood cells were isolated 1 week after the last immunization and the release of IFN- γ (pg/ml) after 72h of antigen stimulation (5
 25 μ g/ml) was measured.
 The values shown are mean of triplicates performed on cells pooled from three mice \pm SEM
- b) - not determined

30 The experiment demonstrates that immunization with the hybrid stimulates T cells which recognize ESAT-6 and MPT59 stronger than after single antigen immunization. Especially the recognition of ESAT-6 was enhanced by immunization with the MPT59-ESAT-6 hybrid. IFN- γ release in control mice immunized with DDA never exceeded 1000 pg/ml.

EXAMPLE 6B

The recombinant antigens were tested individually as subunit vaccines in mice. Eleven groups of 6-8 weeks old, female C57Bl/6j mice (Bomholtegård, Denmark) were immunized subcutaneously at the base of the tail with vaccines of the following composition:

- Group 1: 10 μ g CFP7
- Group 2: 10 μ g CFP17
- Group 3: 10 μ g CFP21
- 10 Group 4: 10 μ g CFP22
- Group 5: 10 μ g CFP25
- Group 6: 10 μ g CFP29
- Group 7: 10 μ g MPT51
- Group 8: 50 μ g ST-CF
- 15 Group 9: Adjuvant control group
- Group 10: BCG $2,5 \times 10^5$ /ml, 0,2 ml
- Group 11: Control group: Untreated

All the subunit vaccines were given with DDA as adjuvant. The animals were vaccinated with a volume of 0.2 ml. Two weeks after the first injection and three weeks after the second injection group 1-9 were boosted a little further up the back. One week after the last injection the mice were bled and the blood cells were isolated. The immune response induced was monitored by release of IFN- γ into the culture supernatant when stimulated in vitro with the homologous protein.

6 weeks after the last immunization the mice were aerosol challenged with 5×10^6 viable *Mycobacterium tuberculosis*/ml. After 6 weeks of infection the mice were killed and the number of viable bacteria in lung and spleen of infected mice was determined by plating serial 3-fold dilutions of organ homogenates on 7H11 plates. Colonies were counted after 2-3 weeks of incubation. The protective efficacy is expressed as the difference between \log_{10} values of the geometric mean of

counts obtained from five mice of the relevant group and the geometric mean of counts obtained from five mouse of the relevant control group.

The results from the experiments are presented in the following table.

Immunogenicity and protective efficacy in mice, of ST-CF and 7 subunit vaccines

	Subunit Vaccine	Immunogenicity	Protective efficacy
	ST-CF	+++	+++
10	CFP7	++	-
	CFP17	+++	+++
	CFP21	+++	++
	CFP22	-	-
	CFP25	+++	+++
15	CFP29	+++	+++
	MPT51	+++	++

+++ Strong immunogen / high protection (level of BCG)
 ++ Medium immunogen / medium protection
 - No recognition / no protection

In conclusion, we have identified a number of proteins inducing high levels of protection. Three of these CFP17, CFP25 and CFP29 giving rise to similar levels of protection as ST-CF and BCG while two proteins CFP21 and MPT51 induces protections around 2/3 the level of BCG and ST-CF. Two of the proteins CFP7 and CFP22 did not induce protection in the mouse model.

EXAMPLE 7

Species distribution of *cfp7*, *cfp9*, *mpt51*, *rdl-orf2*, *rdl-orf3*, *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a* and *rdl-orf9b* as well as of *cfp7a*, *cfp7b*, *cfp10a*, *cfp17*, *cfp20*, *cfp21*, *cfp22*, *cfp22a*, *cfp23*, *cfp25* and *cfp25a*.

tuberculosis-complex and in other mycobacteria PCR and/or Southern blotting was used. The bacterial strains used are listed in TABLE 10. Genomic DNA was prepared from mycobacterial cells as described previously (Andersen et al. 1992).

PCR analyses were used in order to determine the distribution of the *cfp7*, *cfp9* and *mpt51* gene in species belonging to the tuberculosis-complex and in other mycobacteria. The bacterial strains used are listed in TABLE 10. PCR was performed on genomic DNA prepared from mycobacterial cells as described previously (Andersen et al., 1992).

The oligonucleotide primers used were synthesised automatically on a DNA synthesizer (Applied Biosystems, Forster City, Ca, ABI-391, PCR-mode), deblocked, and purified by ethanol precipitation. The primers used for the analyses are shown in TABLE 11.

The PCR amplification was carried out in a thermal reactor (Rapid cycler, Idaho Technology, Idaho) by mixing 20 ng chromosomal with the mastermix (contained 0.5 μ M of each oligonucleotide primer, 0.25 μ M BSA (Stratagene), low salt buffer (20 mM Tris-HCl, pH8.8 , 10 mM KCl, 10 mM $(\text{NH}_4)_2\text{SO}_4$, 2 mM MgSO_4 and 0,1% Triton X-100) (Stratagene), 0.25 mM of each deoxynucleoside triphosphate and 0.5 U Taq Plus Long DNA polymerase (Stratagene)). Final volume was 10 μ l (all concentrations given are concentrations in the final volume).

Predenaturation was carried out at 94°C for 30 s. 30 cycles of the following was performed: Denaturation at 94°C for 30 s, annealing at 55°C for 30 s and elongation at 72°C for 1 min.

The following primer combinations were used (the length of the amplified products are given in parentheses):

- mpt51*: MPT51-3 and MPT51-2 (820 bp), MPT51-3 and MPT51-6 (108 bp), MPT51-5 and MPT51-4 (415 bp), MPT51-7 and MPT51-4 (325 bp).
- cfp7*: pVF1 and PVR1 (274 bp), pVF1 and PVR2 (197 bp), pVF3 and PVR1 (302 bp), pVF3 and PVR2 (125 bp).
- cfp9*: stR3 and stF1 (351 bp).

TABLE 10.
Mycobacterial strains used in this Example.

	Species and strain(s)	Source
	1. <i>M. tuberculosis</i>	H 3 7 R v ATCC ^a (A T C C 27294)
15	2.	H 3 7 R a ATCC (A T C C 25177)
	3.	Erdman Obtained from A. Lazlo, Ottawa, Canada
	4. <i>M. bovis</i> BCG substrain: Danish 1331	SSI ^b
20	5.	Chinese SSI ^c
	6.	Canadian SSI ^c
	7.	Glaxo SSI ^c
	8.	Russia SSI ^c
	9.	Pasteur SSI ^c
25	10.	Japan WHO ^e
	11. <i>M. bovis</i> MNC 27	SSI ^c
	12. <i>M. africanum</i>	Isolated from a Danish patient
	13. <i>M. leprae</i> (armadillo-derived)	Obtained from J. M. Colston, London, UK
	14. <i>M. avium</i> (ATCC 15769)	ATCC
30	15. <i>M. kansasii</i> (ATCC 12478)	ATCC
	16. <i>M. marinum</i> (ATCC 927)	ATCC
	17. <i>M. scrofulaceum</i> (ATCC 19275)	ATCC
	18. <i>M. intercellulare</i> (ATCC 15985)	ATCC
	19. <i>M. fortuitum</i> (ATCC 6841)	ATCC
35	20. <i>M. xenopi</i>	Isolated from a Danish patient
	21. <i>M. flavescens</i>	Isolated from a Danish patient
	22. <i>M. szulgai</i>	Isolated from a Danish patient
	23. <i>M. terrae</i>	SSI ^c
	24. <i>E. coli</i>	SSI ^d
40	25. <i>S. aureus</i>	SSI ^d

^a American Type Culture Collection, USA.

^b Statens Serum Institut, Copenhagen, Denmark.

^c Our collection Department of Mycobacteriology, Statens Serum Institut, Copenhagen, Denmark.

^d Department of Clinical Microbiology, Statens Serum Institut, Denmark.

^e WHO International Laboratory for Biological Standards, Statens Serum Institut, Copenhagen, Denmark.

TABLE 11.

Sequence of the *mpt51*, *cfp7* and *cfp9* oligonucleotides.

Orientation and oligonucleotide		Sequences (5'-3') ^a	Position ^b (nucleotides)
10	Sense		
	MPT51- 1	<u>CTCGAATT</u> CGCCGGTGCACACAG (SEQ ID NO: 28)	6 - 21 (SEQ ID NO: 41)
	MPT51- 3	<u>CTCGAATT</u> CGCCCCATACGAGAAC (SEQ ID NO: 29)	143 - 158 (SEQ ID NO: 41)
15	MPT51- 5	GTGTATCTGCTGGAC (SEQ ID NO: 30)	228 - 242 (SEQ ID NO: 41)
	MPT51- 7	CCGACTGGCTGGCCG (SEQ ID NO: 31)	418 - 432 (SEQ ID NO: 41)
	pvr1	<u>GTACGAGAATT</u> CATGTCGCAAATCATG (SEQ ID NO: 35)	91 - 105 (SEQ ID NO: 1)
20	pvr2	<u>GTACGAGAATT</u> CGAGCTTGGGGTGCCG (SEQ ID NO: 36)	168 - 181 (SEQ ID NO: 1)
	stR3	<u>CGATTCCAAGCTT</u> GTGGCCGCCGACCCG (SEQ ID NO: 37)	141 - 155 (SEQ ID NO: 3)
	Antisense		
	MPT51- 2	GAGGAATT <u>CGCTTAG</u> CGGATCGCA (SEQ ID NO: 32)	946 - 932 (SEQ ID NO: 41)
25	MPT51- 4	CCCACATTCCGTTGG (SEQ ID NO: 33)	642 - 628 (SEQ ID NO: 41)
	MPT51- 6	GTCCAGCAGATACAC (SEQ ID NO: 34)	242 - 228 (SEQ ID NO: 41)
	pVF1	<u>CGTTAGGGATCCT</u> CATCGCCATGGTGTGG (SEQ ID NO: 38)	340 - 323 (SEQ ID NO: 1)
30	pVF3	<u>CGTTAGGGATC</u> CGGTTCCACTGTGCC (SEQ ID NO: 39)	268 - 255 (SEQ ID NO: 1)
	stF1	<u>CGTTAGGGATCCT</u> CAGGTCTTTTCGATG (SEQ ID NO: 40)	467 - 452 (SEQ ID NO: 3)

^a Nucleotides underlined are not contained in the nucleotide sequences of *mpt51*, *cfp7*, and *cfp9*.

^b The positions referred to are of the non-underlined parts of the primers and correspond to the nucleotide sequence shown in SEQ ID NOs: 41, 1, and 3 for *mpt51*, *cfp7*, and *cfp9*, respectively.

35 The Southern blotting was carried out as described previously (Oettinger and Andersen, 1994) with the following modifications: 2 µg of genomic DNA was digested with PvuII, electrophoresed in an 0.8% agarose gel, and transferred onto a nylon membrane (Hybond N-plus; Amersham International plc, Little Chalfont, United Kingdom) with a vacuum transfer device (Milliblot, TM-v; Millipore Corp., Bedford, MA). The *cfp7*,

cfp9, *mpt51*, *rd1-orf2*, *rd1-orf3*, *rd1-orf4*, *rd1-orf5*, *rd1-orf8*, *rd1-orf9a* and *rd1-orf9b* gene fragments were amplified by PCR from the plasmids pRVN01, pRVN02, pT052, pT087, pT088, pT089, pT090, pT091, pT096 or pT098 by using the primers
5 shown in TABLE 11 and TABLE 2 (in Example 2a). The probes were labelled non-radioactively with an enhanced chemiluminescence kit (ECL; Amersham International plc, Little Chalfont, United Kingdom). Hybridization and detection
10 was performed according to the instructions provided by the manufacturer. The results are summarized in TABLES 12 and 13.

TABLE 12. Interspecies analysis of the *cfp7*, *cfp9* and *mpt51* genes by PCR and/or Southern blotting and of MPT51 protein by Western blotting.

Species and strain	PCR			Southern blot			Western blot
	<i>cfp7</i>	<i>cfp9</i>	<i>mpt51</i>	<i>cfp7</i>	<i>cfp9</i>	<i>mpt51</i>	MPT51
1. <i>M. tub.</i> H37Rv	+	+	+	+	+	+	+
5 2. <i>M. tub.</i> H37Ra	+	+	+	N.D.	N.D.	+	+
3. <i>M. tub.</i> Erdmann	+	+	+	+	+	+	+
4. <i>M. bovis</i>	+	+	+			+	+
5. <i>M. bovis</i> BCG Da-nish 1331	+	+	+	+	+	+	+
10 6. <i>M. bovis</i> BCG Japan	+	+	N.D.	+	+	+	N.D.
7. <i>M. bovis</i> BCG Chinese	+	+	N.D.	+	+	N.D.	N.D.
8. <i>M. bovis</i> BCG Canadian	+	+	N.D.	+	+	N.D.	N.D.
15 9. <i>M. bovis</i> BCG Glaxo	+	+	N.D.	+	+	N.D.	N.D.
10. <i>M. bovis</i> BCG Russia	+	+	N.D.	+	+	N.D.	N.D.
20 11. <i>M. bovis</i> BCG Pasteur	+	+	N.D.	+	+	N.D.	N.D.
12. <i>M. africanum</i>	+	+	+	+	+	+	+
13. <i>M. leprae</i>	-	-	-	-	-	-	-
14. <i>M. avium</i>	+	+	-	+	+	+	-
25 15. <i>M. kansasii</i>	+	-	-	+	+	+	-
16. <i>M. marinum</i>	-	(+)	-	+	+	+	-
17. <i>M. scrofulaceum</i>	-	-	-	-	-	-	-
18. <i>M. intercellulare</i>	+	(+)	-	+	+	+	-
30 19. <i>M. fortuitum</i>	-	-	-	-	-	-	-
20. <i>M. flavescens</i>	+	(+)	-	+	+	+	N.D.
21. <i>M. xenopi</i>	-	-	-	N.D.	N.D.	+	-
22. <i>M. szulgai</i>	(+)	(+)	-	-	+	-	-
23. <i>M. terrae</i>	-	-	N.D.	N.D.	N.D.	N.D.	N.D.
35 +, positive reaction; -, no reaction, N.D. not determined.							

cfp7, *cfp9* and *mpt51* were found in the *M. tuberculosis* complex including BCG and the environmental mycobacteria; *M. avium*, *M. kansasii*, *M. marinum*, *M. intracellular* and *M. flavescens*. *cfp9* was additionally found in *M. szulgai* and *mpt51* in *M. xenopi*.

Furthermore the presence of native MPT51 in culture filtrates from different mycobacterial strains was investigated with western blots developed with Mab HBT4.

There is a strong band at around 26 kDa in *M. tuberculosis* H37Rv, Ra, Erdman, *M. bovis* AN5, *M. bovis* BCG substrain Danish 1331 and *M. africanum*. No band was seen in the region in any other tested mycobacterial strains.

TABLE 13a. Interspecies analysis of the *rd1-orf2*, *rd1-orf3*, *rd1-orf4*, *rd1-orf5*, *rd1-orf8*, *rd1-orf9a* and *rd1-orf9b* genes by Southern blotting.

Species and strain	<i>rd1-orf2</i>	<i>rd1-orf3</i>	<i>rd1-orf4</i>	<i>rd1-orf5</i>	<i>rd1-orf8</i>	<i>rd1-orf9a</i>	<i>rd1-orf9b</i>
1. <i>M. tub.</i> H37Rv	+	+	+	+	+	+	+
2. <i>M. bovis</i>	+	+	+	+	N.D.	+	+
3. <i>M. bovis</i> BCG Danish 1331	+	-	-	-	N.D.	-	-
4. <i>M. bovis</i> BCG Japan	+	-	-	-	N.D.	-	-
5. <i>M. avium</i>	-	-	-	-	N.D.	-	-
6. <i>M. kansasii</i>	-	-	-	-	N.D.	-	-
7. <i>M. marinum</i>	+	-	+	-	N.D.	-	-
8. <i>M. scrofulaceum</i>	+	-	-	-	N.D.	-	-
9. <i>M. intercellulare</i>	-	-	-	-	N.D.	-	-
10. <i>M. fortuitum</i>	-	-	-	-	N.D.	-	-
11. <i>M. xenopi</i>	-	-	-	-	N.D.	-	-
12. <i>M. szulgai</i>	+	-	-	-	N.D.	-	-
+, positive reaction; -, no reaction, N.D. not determined.							

Positive results for *rd1-orf2*, *rd1-orf3*, *rd1-orf4*, *rd1-orf5*, *rd1-orf8*, *rd1-orf9a* and *rd1-orf9b* were only obtained when using genomic DNA from *M. tuberculosis* and *M. bovis*, and not from *M. bovis* BCG or other mycobacteria analyzed except *rd1-orf4* which also was found in *M. marinum*.

Presence of *cfp7a*, *cfp7b*, *cfp10a*, *cfp17*, *cfp20*, *cfp21*, *cfp22*, *cfp22a*, *cfp23*, *cfp25* and *cfp25a* in different mycobacterial species.

Southern blotting was carried out as described for *rdl-orf2*, *rdl-orf3*, *rdl-orf4*, *rdl-orf5*, *rdl-orf8*, *rdl-orf9a* and *rdl-orf9b*. The *cfp7a*, *cfp7b*, *cfp10a*, *cfp17*, *cfp20*, *cfp21*, *cfp22*, *cfp22a*, *cfp23*, *cfp25* and *cfp25a* gene fragments were amplified
 5 by PCR from the recombinant pMCT6 plasmids encoding the individual genes. The primers used (same as the primers used for cloning) are described in example 3, 3A and 3B. The results are summarized in Table 13b.

10 **TABLE 13b.** Interspecies analysis of the *cfp7a*, *cfp7b*, *cfp10a*, *cfp17*, *cfp20*, *cfp21*, *cfp22*, *cfp22a*, *cfp23*, *cfp25*, and *cfp25a* genes by Southern blotting.

Species and strain	<i>cfp7a</i>	<i>cfp7b</i>	<i>cfp10a</i>	<i>cfp17</i>	<i>cfp20</i>	<i>cfp21</i>	<i>cfp22</i>	<i>cfp22a</i>	<i>cfp23</i>	<i>cfp25</i>	<i>cfp25a</i>
1. <i>M. tub.</i> H37Rv	+	+	+	+	+	+	+	+	+	+	+
2. <i>M. bovis</i>	+	+	+	+	+	+	+	+	+	+	+
3. <i>M. bovis</i> BCG	+	+	+	+	+	N.D.	+	+	+	+	+
15 Danish 1331											
4. <i>M. bovis</i> BCG Japan	+	+	+	+	+	+	+	+	+	+	+
5. <i>M. avium</i>	+	N.D.	-	+	-	+	+	+	+	+	-
6. <i>M. kansasii</i>	-	N.D.	+	-	-	-	+	-	+	-	-
20 7. <i>M. marinum</i>	+	+	-	+	+	+	+	+	+	+	+
8. <i>M. scrofulaceum</i>	-	-	+	-	+	+	-	+	+	+	-
9. <i>M. intercellulare</i>	+	+	-	+	-	+	+	-	+	+	-
10. <i>M. fortuitum</i>	-	N.D.	-	-	-	-	-	-	+	-	-
11. <i>M. xenopi</i>	+	+	+	+	+	+	+	+	+	+	+
25 12. <i>M. szulgai</i>	+	+	-	+	+	+	+	+	+	+	+

+, positive reaction; -, no reaction, N.D. not determined.

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(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 91..381

(ix) FEATURE:

- (A) NAME/KEY: -35_signal
- (B) LOCATION: 14..19

(ix) FEATURE:

- (A) NAME/KEY: -10_signal
- (B) LOCATION: 47..50

(ix) FEATURE:

- (A) NAME/KEY: RBS
- (B) LOCATION: 78..84

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 91..381

123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GGCCGCCGGT ACCTATGTGG CCGCCGATGC TCGGGACGCG TCGACCTATA CCGGGTTCTG      60
ATCGAACCCT GCTGACCGAG AGGACTTGTG ATG TCG CAA ATC ATG TAC AAC TAC      114
                Met Ser Gln Ile Met Tyr Asn Tyr
                  1                      5

CCC GCG ATG TTG GGT CAC GCC GGG GAT ATG GCC GGA TAT GCC GGC ACG      162
Pro Ala Met Leu Gly His Ala Gly Asp Met Ala Gly Tyr Ala Gly Thr
    10                      15                      20

CTG CAG AGC TTG GGT GCC GAG ATC GCC GTG GAG CAG GCC GCG TTG CAG      210
Leu Gln Ser Leu Gly Ala Glu Ile Ala Val Glu Gln Ala Ala Leu Gln
    25                      30                      35                      40

AGT GCG TGG CAG GGC GAT ACC GGG ATC ACG TAT CAG GCG TGG CAG GCA      258
Ser Ala Trp Gln Gly Asp Thr Gly Ile Thr Tyr Gln Ala Trp Gln Ala
                45                      50                      55

CAG TGG AAC CAG GCC ATG GAA GAT TTG GTG CGG GCC TAT CAT GCG ATG      306
Gln Trp Asn Gln Ala Met Glu Asp Leu Val Arg Ala Tyr His Ala Met
                60                      65                      70

TCC AGC ACC CAT GAA GCC AAC ACC ATG GCG ATG ATG GCC CGC GAC ACC      354
Ser Ser Thr His Glu Ala Asn Thr Met Ala Met Met Ala Arg Asp Thr
    75                      80                      85

GCC GAA GCC GCC AAA TGG GGC GGC TAG      381
Ala Glu Ala Ala Lys Trp Gly Gly
    90                      95

```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Ser Gln Ile Met Tyr Asn Tyr Pro Ala Met Leu Gly His Ala Gly
  1                      5                      10                      15
Asp Met Ala Gly Tyr Ala Gly Thr Leu Gln Ser Leu Gly Ala Glu Ile
    20                      25                      30
Ala Val Glu Gln Ala Ala Leu Gln Ser Ala Trp Gln Gly Asp Thr Gly
    35                      40                      45
Ile Thr Tyr Gln Ala Trp Gln Ala Gln Trp Asn Gln Ala Met Glu Asp
    50                      55                      60
Leu Val Arg Ala Tyr His Ala Met Ser Ser Thr His Glu Ala Asn Thr
    65                      70                      75                      80

```

Met Ala Met Met Ala Arg Asp Thr Ala Glu Ala Ala Lys Trp Gly Gly
85 90 95

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(A) NAME/KEY: CDS
(B) LOCATION: 141..467

(A) NAME/KEY: -10_signal
(B) LOCATION: 73..78

(A) NAME/KEY: -35_signal
(B) LOCATION: 4..9

(A) NAME/KEY: RBS
(B) LOCATION: 123..130

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(A) NAME/KEY: mat_peptide
(B) LOCATION: 141..467
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GGGTAGCCGG	ACCACGGCTG	GGCAAAGATG	TGCAGGCCGC	CATCAAGGCG	GTCAAGGCCG		60
GCGACGGCGT	CATAAACCCG	GACGGCACCT	TGTTGGCGGG	CCCCGCGGTG	CTGACGCCCC		120
ACGAGTACAA	CTCCCGGCTG	GTG	GCC	GCC	GAC	CCG	170
		Met	Ala	Ala	Asp	Pro	
		1				5	
							10
TTG	CCC	GAC	GGC	GCC	GGG	CTG	218
Leu	Pro	Asp	Gly	Ala	Gly	Leu	
			15			20	
							25
GAA	CTC	GAA	GCC	GAG	GGC	TGG	266
Glu	Leu	Glu	Ala	Glu	Gly	Trp	
			30			35	
							40

125

GAG CTG CGT AAG TCG ACC GGG CTG GAC GTT TCC GAC CGC ATC CGG GTG	314
Glu Leu Arg Lys Ser Thr Gly Leu Asp Val Ser Asp Arg Ile Arg Val	
45 50 55	
GTG ATG TCG GTG CCT GCG GAA CGC GAA GAC TGG GCG CGC ACC CAT CGC	362
Val Met Ser Val Pro Ala Glu Arg Glu Asp Trp Ala Arg Thr His Arg	
60 65 70	
GAC CTC ATT GCC GGA GAA ATC TTG GCT ACC GAC TTC GAA TTC GCC GAC	410
Asp Leu Ile Ala Gly Glu Ile Leu Ala Thr Asp Phe Glu Phe Ala Asp	
75 80 85 90	
CTC GCC GAT GGT GTG GCC ATC GGC GAC GGC GTG CGG GTA AGC ATC GAA	458
Leu Ala Asp Gly Val Ala Ile Gly Asp Gly Val Arg Val Ser Ile Glu	
95 100 105	
AAG ACC TGA	467
Lys Thr	

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Ala Asp Pro Glu Ser Thr Ala Ala Leu Pro Asp Gly Ala Gly	
1 5 10 15	
Leu Val Val Leu Asp Gly Thr Val Thr Ala Glu Leu Glu Ala Glu Gly	
20 25 30	
Trp Ala Lys Asp Arg Ile Arg Glu Leu Gln Glu Leu Arg Lys Ser Thr	
35 40 45	
Gly Leu Asp Val Ser Asp Arg Ile Arg Val Val Met Ser Val Pro Ala	
50 55 60	
Glu Arg Glu Asp Trp Ala Arg Thr His Arg Asp Leu Ile Ala Gly Glu	
65 70 75 80	
Ile Leu Ala Thr Asp Phe Glu Phe Ala Asp Leu Ala Asp Gly Val Ala	
85 90 95	
Ile Gly Asp Gly Val Arg Val Ser Ile Glu Lys Thr	
100 105	

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 889 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

126

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(B) STRAIN: H37Rv

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 201..689

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 201..290

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 291..689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CGGGTCTGCA CGGATCCGGG CCGGGCAGGG CAATCGAGCC TGGGATCCGC TGGGGTGCGC	60
ACATCGCGGA CCCGTGCGCG GTACGGTCGA GACAGCGGCA CGAGAAAGTA GTAAGGGCGA	120
TAATAGGCGG TAAAGAGTAG CGGGAAGCCG GCCGAACGAC TCGGTCAGAC AACGCCACAG	180
CGGCCAGTGA GGAGCAGCGG GTG ACG GAC ATG AAC CCG GAT ATT GAG AAG	230
Met Thr Asp Met Asn Pro Asp Ile Glu Lys	
-30 -25	
GAC CAG ACC TCC GAT GAA GTC ACG GTA GAG ACG ACC TCC GTC TTC CGC	278
Asp Gln Thr Ser Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg	
-20 -15 -10 -5	
GCA GAC TTC CTC AGC GAG CTG GAC GCT CCT GCG CAA GCG GGT ACG GAG	326
Ala Asp Phe Leu Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu	
1 5 10	
AGC GCG GTC TCC GGG GTG GAA GGG CTC CCG CCG GGC TCG GCG TTG CTG	374
Ser Ala Val Ser Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu	
15 20 25	
GTA GTC AAA CGA GGC CCC AAC GCC GGG TCC CCG TTC CTA CTC GAC CAA	422
Val Val Lys Arg Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln	
30 35 40	
GCC ATC ACG TCG GCT GGT CGG CAT CCC GAC AGC GAC ATA TTT CTC GAC	470
Ala Ile Thr Ser Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp	
45 50 55 60	
GAC GTG ACC GTG AGC CGT CGC CAT GCT GAA TTC CGG TTG GAA AAC AAC	518
Asp Val Thr Val Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn	
65 70 75	

127

GAA TTC AAT GTC GTC GAT GTC GGG AGT CTC AAC GGC ACC TAC GTC AAC	566
Glu Phe Asn Val Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn	
80 85 90	
CGC GAG CCC GTG GAT TCG GCG GTG CTG GCG AAC GGC GAC GAG GTC CAG	614
Arg Glu Pro Val Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln	
95 100 105	
ATC GGC AAG TTC CGG TTG GTG TTC TTG ACC GGA CCC AAG CAA GGC GAG	662
Ile Gly Lys Phe Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu	
110 115 120	
GAT GAC GGG AGT ACC GGG GGC CCG TGA GCGCACCCGA TAGCCCCGCG	709
Asp Asp Gly Ser Thr Gly Gly Pro	
125 130	
CTGGCCGGGA TGTCGATCGG GGCGGTCTC GACCTGCTAC GACCGGATTT TCCTGATGTC	769
ACCATCTCCA AGATTCGATT CTTGGAGGCT GAGGGTCTGG TGACGCCCCG GCGGGCCTCA	829
TCGGGGTATC GGCGGTTTAC CGCATACGAC TGCGCACGGC TGCGATTTCAT TCTCACTGCC	889

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Thr Asp Met Asn Pro Asp Ile Glu Lys Asp Gln Thr Ser Asp Glu	
-30 -25 -20 -15	
Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu Ser Glu	
-10 -5 1	
Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser Gly Val	
5 10 15	
Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg Gly Pro	
20 25 30	
Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser Ala Gly	
35 40 45 50	
Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val Ser Arg	
55 60 65	
Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val Val Asp	
70 75 80	
Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val Asp Ser	
85 90 95	

Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Phe Arg Leu
 100 105 110

Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser Thr Gly
 115 120 125 130

Gly Pro

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..698

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 201..698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCGACTCCGG CGCCACCGGG CAGGATCACG GTGTCGACGG GGTCGCCGGG GAATCCCACG	60
ATAACCACTC TTCGCGCCAT GAATGCCAGT GTTGGCCAGG CGCTGGCCTG GCGTCCACGC	120
CACACACCGC ACAGATTAGG ACACGCCGGC GGCGCAGCCC TGCCCGAAAG ACCGTGCACC	180
GGTCTTGCCA GACTGTGCCC ATG GCA CAG ATA ACC CTG CGA GGA AAC GCG	230
Met Ala Gln Ile Thr Leu Arg Gly Asn Ala	
1 5 10	
ATC AAT ACC GTC GGT GAG CTA CCT GCT GTC GGA TCC CCG GCC CCG GCC	278
Ile Asn Thr Val Gly Glu Leu Pro Ala Val Gly Ser Pro Ala Pro Ala	
15 20 25	
TTC ACC CTG ACC GGG GGC GAT CTG GGG GTG ATC AGC AGC GAC CAG TTC	326
Phe Thr Leu Thr Gly Gly Asp Leu Gly Val Ile Ser Ser Asp Gln Phe	
30 35 40	
CGG GGT AAG TCC GTG TTG CTG AAC ATC TTT CCA TCC GTG GAC ACA CCG	374
Arg Gly Lys Ser Val Leu Leu Asn Ile Phe Pro Ser Val Asp Thr Pro	
45 50 55	

129

GTG TGC GCG ACG AGT GTG CGA ACC TTC GAC GAG CGT GCG GCG GCA AGT	422
Val Cys Ala Thr Ser Val Arg Thr Phe Asp Glu Arg Ala Ala Ala Ser	
60 65 70	
GGC GCT ACC GTG CTG TGT GTC TCG AAG GAT CTG CCG TTC GCC CAG AAG	470
Gly Ala Thr Val Leu Cys Val Ser Lys Asp Leu Pro Phe Ala Gln Lys	
75 80 85 90	
CGC TTC TGC GGC GCC GAG GGC ACC GAA AAC GTC ATG CCC GCG TCG GCA	518
Arg Phe Cys Gly Ala Glu Gly Thr Glu Asn Val Met Pro Ala Ser Ala	
95 100 105	
TTC CGG GAC AGC TTC GGC GAG GAT TAC GGC GTG ACC ATC GCC GAC GGG	566
Phe Arg Asp Ser Phe Gly Glu Asp Tyr Gly Val Thr Ile Ala Asp Gly	
110 115 120	
CCG ATG GCC GGG CTG CTC GCC CGC GCA ATC GTG GTG ATC GGC GCG GAC	614
Pro Met Ala Gly Leu Leu Ala Arg Ala Ile Val Val Ile Gly Ala Asp	
125 130 135	
GGC AAC GTC GCC TAC ACG GAA TTG GTG CCG GAA ATC GCG CAA GAA CCC	662
Gly Asn Val Ala Tyr Thr Glu Leu Val Pro Glu Ile Ala Gln Glu Pro	
140 145 150	
AAC TAC GAA GCG GCG CTG GCC GCG CTG GGC GCC TAG GCTTTCACAA	708
Asn Tyr Glu Ala Ala Leu Ala Ala Leu Gly Ala	
155 160 165	
GCCCCGCGCG TTCGGCGAGC AGCGCACGAT TTCGAGCGCT GCTCCCGAAA AGCGCCTCGG	768
TGGTCTTGGC CCGGCGGTAA TACAGGTGCA GGTCGTGCTC CCACGTGAAG GCGATGGCAC	828
CGTGGATCTG AAGAGCGGAG CCGGCGCATA ACACAAAGGT TTCCGCGGTC TGCGCCTTCG	888
CCAGCGGCGC	898

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Ala Gln Ile Thr Leu Arg Gly Asn Ala Ile Asn Thr Val Gly Glu	
1 5 10 15	
Leu Pro Ala Val Gly Ser Pro Ala Pro Ala Phe Thr Leu Thr Gly Gly	
20 25 30	
Asp Leu Gly Val Ile Ser Ser Asp Gln Phe Arg Gly Lys Ser Val Leu	
35 40 45	
Leu Asn Ile Phe Pro Ser Val Asp Thr Pro Val Cys Ala Thr Ser Val	
50 55 60	

130

Arg Thr Phe Asp Glu Arg Ala Ala Ala Ser Gly Ala Thr Val Leu Cys
 65 70 75 80
 Val Ser Lys Asp Leu Pro Phe Ala Gln Lys Arg Phe Cys Gly Ala Glu
 85 90 95
 Gly Thr Glu Asn Val Met Pro Ala Ser Ala Phe Arg Asp Ser Phe Gly
 100 105 110
 Glu Asp Tyr Gly Val Thr Ile Ala Asp Gly Pro Met Ala Gly Leu Leu
 115 120 125
 Ala Arg Ala Ile Val Val Ile Gly Ala Asp Gly Asn Val Ala Tyr Thr
 130 135 140
 Glu Leu Val Pro Glu Ile Ala Gln Glu Pro Asn Tyr Glu Ala Ala Leu
 145 150 155 160
 Ala Ala Leu Gly Ala
 165

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1054 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..854

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 201..296

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 297..854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATAATCAGCT CACCGTTGGG ACCGACCTCG ACCAGGGGTC CTTTGTGACT GCCGGGCTTG 60
 ACGCGGACGA CCACAGAGTC GGTCATCGCC TAAGGCTACC GTTCTGACCT GGGGCTGCGT 120
 GGGCGCCGAC GACGTGAGGC ACGTCATGTC TCAGCGGCCC ACCGCCACCT CGGTCGCCGG 180

131

CAGTATGTCA GCATGTGCAG ATG ACT CCA CGC AGC CTT GTT CGC ATC GTT	230
Met Thr Pro Arg Ser Leu Val Arg Ile Val	
-32 -30 -25	
GGT GTC GTG GTT GCG ACG ACC TTG GCG CTG GTG AGC GCA CCC GCC GGC	278
Gly Val Val Val Ala Thr Thr Leu Ala Leu Val Ser Ala Pro Ala Gly	
-20 -15 -10	
GGT CGT GCC GCG CAT GCG GAT CCG TGT TCG GAC ATC GCG GTC GTT TTC	326
Gly Arg Ala Ala His Ala Asp Pro Cys Ser Asp Ile Ala Val Val Phe	
-5 1 5 10	
GCT CGC GGC ACG CAT CAG GCT TCT GGT CTT GGC GAC GTC GGT GAG GCG	374
Ala Arg Gly Thr His Gln Ala Ser Gly Leu Gly Asp Val Gly Glu Ala	
15 20 25	
TTC GTC GAC TCG CTT ACC TCG CAA GTT GGC GGG CGG TCG ATT GGG GTC	422
Phe Val Asp Ser Leu Thr Ser Gln Val Gly Gly Arg Ser Ile Gly Val	
30 35 40	
TAC GCG GTG AAC TAC CCA GCA AGC GAC GAC TAC CGC GCG AGC GCG TCA	470
Tyr Ala Val Asn Tyr Pro Ala Ser Asp Asp Tyr Arg Ala Ser Ala Ser	
45 50 55	
AAC GGT TCC GAT GAT GCG AGC GCC CAC ATC CAG CGC ACC GTC GCC AGC	518
Asn Gly Ser Asp Asp Ala Ser Ala His Ile Gln Arg Thr Val Ala Ser	
60 65 70	
TGC CCG AAC ACC AGG ATT GTG CTT GGT GGC TAT TCG CAG GGT GCG ACG	566
Cys Pro Asn Thr Arg Ile Val Leu Gly Gly Tyr Ser Gln Gly Ala Thr	
75 80 85 90	
GTC ATC GAT TTG TCC ACC TCG GCG ATG CCG CCC GCG GTG GCA GAT CAT	614
Val Ile Asp Leu Ser Thr Ser Ala Met Pro Pro Ala Val Ala Asp His	
95 100 105	
GTC GCC GCT GTC GCC CTT TTC GGC GAG CCA TCC AGT GGT TTC TCC AGC	662
Val Ala Ala Val Ala Leu Phe Gly Glu Pro Ser Ser Gly Phe Ser Ser	
110 115 120	
ATG TTG TGG GGC GGC GGG TCG TTG CCG ACA ATC GGT CCG CTG TAT AGC	710
Met Leu Trp Gly Gly Gly Ser Leu Pro Thr Ile Gly Pro Leu Tyr Ser	
125 130 135	
TCT AAG ACC ATA AAC TTG TGT GCT CCC GAC GAT CCA ATA TGC ACC GGA	758
Ser Lys Thr Ile Asn Leu Cys Ala Pro Asp Asp Pro Ile Cys Thr Gly	
140 145 150	
GGC GGC AAT ATT ATG GCG CAT GTT TCG TAT GTT CAG TCG GGG ATG ACA	806
Gly Gly Asn Ile Met Ala His Val Ser Tyr Val Gln Ser Gly Met Thr	
155 160 165 170	
AGC CAG GCG GCG ACA TTC GCG GCG AAC AGG CTC GAT CAC GCC GGA TGA	854
Ser Gln Ala Ala Thr Phe Ala Ala Asn Arg Leu Asp His Ala Gly	
175 180 185	
TCAAAGACTG TTGTCCCTAT ACCGCTGGGG CTGTAGTCGA TGTACACCGG CTGGAATCTG	914

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AAGGGCAAGA ACCCGGTATT CATCAGGCCG GATGAAATGA CGGTCGGGCG GTAATCGTTT 974
 GTGTTGAACG CGTAGAGCCG ATCACCGCCG GGGCTGGTGT AGACCTCAAT GTTTGTGTTC 1034
 GCCGGCAGGG TTCCGGATCC 1054

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Thr Pro Arg Ser Leu Val Arg Ile Val Gly Val Val Val Ala Thr
 -32 -30 -25 -20

Thr Leu Ala Leu Val Ser Ala Pro Ala Gly Gly Arg Ala Ala His Ala
 -15 -10 -5

Asp Pro Cys Ser Asp Ile Ala Val Val Phe Ala Arg Gly Thr His Gln
 1 5 10 15

Ala Ser Gly Leu Gly Asp Val Gly Glu Ala Phe Val Asp Ser Leu Thr
 20 25 30

Ser Gln Val Gly Gly Arg Ser Ile Gly Val Tyr Ala Val Asn Tyr Pro
 35 40 45

Ala Ser Asp Asp Tyr Arg Ala Ser Ala Ser Asn Gly Ser Asp Asp Ala
 50 55 60

Ser Ala His Ile Gln Arg Thr Val Ala Ser Cys Pro Asn Thr Arg Ile
 65 70 75 80

Val Leu Gly Gly Tyr Ser Gln Gly Ala Thr Val Ile Asp Leu Ser Thr
 85 90 95

Ser Ala Met Pro Pro Ala Val Ala Asp His Val Ala Ala Val Ala Leu
 100 105 110

Phe Gly Glu Pro Ser Ser Gly Phe Ser Ser Met Leu Trp Gly Gly Gly
 115 120 125

Ser Leu Pro Thr Ile Gly Pro Leu Tyr Ser Ser Lys Thr Ile Asn Leu
 130 135 140

Cys Ala Pro Asp Asp Pro Ile Cys Thr Gly Gly Gly Asn Ile Met Ala
 145 150 155 160

His Val Ser Tyr Val Gln Ser Gly Met Thr Ser Gln Ala Ala Thr Phe
 165 170 175

Ala Ala Asn Arg Leu Asp His Ala Gly
 180 185

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 949 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..749

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 224..749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

AGCCGCTCGC GTGGGGTCAA CCGGGTTTCC ACCTGCTCAC TCATTTTGCC GCCTTTCTGT      60
GTCCGGGGCCG AGGCTTGCGC TCAATAACTC GGTCAAGTTC CTTACAGAC TGCCATCACT      120
GGCCCGTCGG CGGGCTCGTT GCGGGTGCGC CGCGTGCGGG TTTGTGTTCC GGGCACCGGG      180
TGGGGGCCCCG CCCGGGCGTA ATG GCA GAC TGT GAT TCC GTG ACT AAC AGC          230
      Met Ala Asp Cys Asp Ser Val Thr Asn Ser
      -7      -5                      1

CCC CTT GCG ACC GCT ACC GCC ACG CTG CAC ACT AAC CGC GGC GAC ATC          278
Pro Leu Ala Thr Ala Thr Ala Thr Leu His Thr Asn Arg Gly Asp Ile
      5              10              15

AAG ATC GCC CTG TTC GGA AAC CAT GCG CCC AAG ACC GTC GCC AAT TTT          326
Lys Ile Ala Leu Phe Gly Asn His Ala Pro Lys Thr Val Ala Asn Phe
      20              25              30              35

GTG GGC CTT GCG CAG GGC ACC AAG GAC TAT TCG ACC CAA AAC GCA TCA          374
Val Gly Leu Ala Gln Gly Thr Lys Asp Tyr Ser Thr Gln Asn Ala Ser
              40              45              50

GGT GGC CCG TCC GGC CCG TTC TAC GAC GGC GCG GTC TTT CAC CGG GTG          422
Gly Gly Pro Ser Gly Pro Phe Tyr Asp Gly Ala Val Phe His Arg Val
              55              60              65

ATC CAG GGC TTC ATG ATC CAG GGT GGC GAT CCA ACC GGG ACG GGT CGC          470
Ile Gln Gly Phe Met Ile Gln Gly Gly Asp Pro Thr Gly Thr Gly Arg
              70              75              80

GGC GGA CCC GGC TAC AAG TTC GCC GAC GAG TTC CAC CCC GAG CTG CAA          518
Gly Gly Pro Gly Tyr Lys Phe Ala Asp Glu Phe His Pro Glu Leu Gln
      85              90              95

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TTC GAC AAG CCC TAT CTG CTC GCG ATG GCC AAC GCC GGT CCG GGC ACC	566
Phe Asp Lys Pro Tyr Leu Leu Ala Met Ala Asn Ala Gly Pro Gly Thr	
100 105 110 115	
AAC GGC TCA CAG TTT TTC ATC ACC GTC GGC AAG ACT CCG CAC CTG AAC	614
Asn Gly Ser Gln Phe Phe Ile Thr Val Gly Lys Thr Pro His Leu Asn	
120 125 130	
CGG CGC CAC ACC ATT TTC GGT GAA GTG ATC GAC GCG GAG TCA CAG CGG	662
Arg Arg His Thr Ile Phe Gly Glu Val Ile Asp Ala Glu Ser Gln Arg	
135 140 145	
GTT GTG GAG GCG ATC TCC AAG ACG GCC ACC GAC GGC AAC GAT CGG CCG	710
Val Val Glu Ala Ile Ser Lys Thr Ala Thr Asp Gly Asn Asp Arg Pro	
150 155 160	
ACG GAC CCG GTG GTG ATC GAG TCG ATC ACC ATC TCC TGA CCCGAAGCTA	759
Thr Asp Pro Val Val Ile Glu Ser Ile Thr Ile Ser	
165 170 175	
CGTCGGCTCG TCGCTCGAAT ACACCTTGTTG GACCCGCCAG GGCACGTGGC GGTACACCGA	819
CACGCCGTTG GGGCCGTTCA ACCGGACGCC CTCACGCCAA GTCCGCTCAC CTTTGGCCGC	879
GACCGGCGTA ACCGGCAGCG GTAAGCGCAT CGAGCACCTC CACTGGGTCG GTGCCGAGAT	939
CCCAGCGGGA	949

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ala Asp Cys Asp Ser Val Thr Asn Ser Pro Leu Ala Thr Ala Thr	
-7 -5 1 5	
Ala Thr Leu His Thr Asn Arg Gly Asp Ile Lys Ile Ala Leu Phe Gly	
10 15 20 25	
Asn His Ala Pro Lys Thr Val Ala Asn Phe Val Gly Leu Ala Gln Gly	
30 35 40	
Thr Lys Asp Tyr Ser Thr Gln Asn Ala Ser Gly Gly Pro Ser Gly Pro	
45 50 55	
Phe Tyr Asp Gly Ala Val Phe His Arg Val Ile Gln Gly Phe Met Ile	
60 65 70	
Gln Gly Gly Asp Pro Thr Gly Thr Gly Arg Gly Gly Pro Gly Tyr Lys	
75 80 85	

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Phe Ala Asp Glu Phe His Pro Glu Leu Gln Phe Asp Lys Pro Tyr Leu
 90 95 100 105
 Leu Ala Met Ala Asn Ala Gly Pro Gly Thr Asn Gly Ser Gln Phe Phe
 110 115 120
 Ile Thr Val Gly Lys Thr Pro His Leu Asn Arg Arg His Thr Ile Phe
 125 130 135
 Gly Glu Val Ile Asp Ala Glu Ser Gln Arg Val Val Glu Ala Ile Ser
 140 145 150
 Lys Thr Ala Thr Asp Gly Asn Asp Arg Pro Thr Asp Pro Val Val Ile
 155 160 165
 Glu Ser Ile Thr Ile Ser
 170 175

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..860

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 201..296

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 297..860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TGGACCTTCA CCGGCGGTCC CTTCGCTTCG GGGGCGACAC CTAACATACT GGTTCGTCAAC	60
CTACCGCGAC ACCGCTGGGA CTTTGTGCCA TTGCCGGCCA CTCGGGGCCG CTGCGGCCTG	120
GAAAAATTGG TCGGGCACGG GCGGCCGCGG GTCGCTACCA TCCCACTGTG AATGATTTAC	180
TGACCCGCCG ACTGCTCACC ATG GGC GCG GCC GCC GCA ATG CTG GCC GCG	230
Met Gly Ala Ala Ala Ala Met Leu Ala Ala	
-32 -30 -25	

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GTG	CTT	CTG	CTT	ACT	CCC	ATC	ACC	GTT	CCC	GCC	GGC	TAC	CCC	GGT	GCC	278
Val	Leu	Leu	Leu	Thr	Pro	Ile	Thr	Val	Pro	Ala	Gly	Tyr	Pro	Gly	Ala	
		-20					-15					-10				
GTT	GCA	CCG	GCC	ACT	GCA	GCC	TGC	CCC	GAC	GCC	GAA	GTG	GTG	TTC	GCC	326
Val	Ala	Pro	Ala	Thr	Ala	Ala	Cys	Pro	Asp	Ala	Glu	Val	Val	Phe	Ala	
	-5					1				5					10	
CGC	GGC	CGC	TTC	GAA	CCG	CCC	GGG	ATT	GGC	ACG	GTC	GGC	AAC	GCA	TTC	374
Arg	Gly	Arg	Phe	Glu	Pro	Pro	Gly	Ile	Gly	Thr	Val	Gly	Asn	Ala	Phe	
				15				20						25		
GTC	AGC	GCG	CTG	CGC	TCG	AAG	GTC	AAC	AAG	AAT	GTC	GGG	GTC	TAC	GCG	422
Val	Ser	Ala	Leu	Arg	Ser	Lys	Val	Asn	Lys	Asn	Val	Gly	Val	Tyr	Ala	
			30				35						40			
GTG	AAA	TAC	CCC	GCC	GAC	AAT	CAG	ATC	GAT	GTG	GGC	GCC	AAC	GAC	ATG	470
Val	Lys	Tyr	Pro	Ala	Asp	Asn	Gln	Ile	Asp	Val	Gly	Ala	Asn	Asp	Met	
	45					50					55					
AGC	GCC	CAC	ATT	CAG	AGC	ATG	GCC	AAC	AGC	TGT	CCG	AAT	ACC	CGC	CTG	518
Ser	Ala	His	Ile	Gln	Ser	Met	Ala	Asn	Ser	Cys	Pro	Asn	Thr	Arg	Leu	
	60					65				70						
GTG	CCC	GGC	GGT	TAC	TCG	CTG	GGC	GCG	GCC	GTC	ACC	GAC	GTG	GTA	CTC	566
Val	Pro	Gly	Gly	Tyr	Ser	Leu	Gly	Ala	Ala	Val	Thr	Asp	Val	Val	Leu	
	75				80					85					90	
GCG	GTG	CCC	ACC	CAG	ATG	TGG	GGC	TTC	ACC	AAT	CCC	CTG	CCT	CCC	GGC	614
Ala	Val	Pro	Thr	Gln	Met	Trp	Gly	Phe	Thr	Asn	Pro	Leu	Pro	Pro	Gly	
				95				100						105		
AGT	GAT	GAG	CAC	ATC	GCC	GCG	GTC	GCG	CTG	TTC	GGC	AAT	GGC	AGT	CAG	662
Ser	Asp	Glu	His	Ile	Ala	Ala	Val	Ala	Leu	Phe	Gly	Asn	Gly	Ser	Gln	
			110				115						120			
TGG	GTC	GGC	CCC	ATC	ACC	AAC	TTC	AGC	CCC	GCC	TAC	AAC	GAT	CGG	ACC	710
Trp	Val	Gly	Pro	Ile	Thr	Asn	Phe	Ser	Pro	Ala	Tyr	Asn	Asp	Arg	Thr	
		125				130						135				
ATC	GAG	TTG	TGT	CAC	GGC	GAC	GAC	CCC	GTC	TGC	CAC	CCT	GCC	GAC	CCC	758
Ile	Glu	Leu	Cys	His	Gly	Asp	Asp	Pro	Val	Cys	His	Pro	Ala	Asp	Pro	
	140					145					150					
AAC	ACC	TGG	GAG	GCC	AAC	TGG	CCC	CAG	CAC	CTC	GCC	GGG	GCC	TAT	GTC	806
Asn	Thr	Trp	Glu	Ala	Asn	Trp	Pro	Gln	His	Leu	Ala	Gly	Ala	Tyr	Val	
	155				160					165				170		
TCG	TCG	GGC	ATG	GTC	AAC	CAG	GCG	GCT	GAC	TTC	GTT	GCC	GGA	AAG	CTG	854
Ser	Ser	Gly	Met	Val	Asn	Gln	Ala	Ala	Asp	Phe	Val	Ala	Gly	Lys	Leu	
			175				180						185			
CAA	TAG	CCACCTAGCC	CGTGCGCGAG	TCTTTGCTTC	ACGCTTTCGC	TAACCGACCA										910
Gln																
ACGCGCGCAC	GATGGAGGGG	TCCGTGGTCA	TATCAAGACA	AGAAGGGAGT	AGGCGATGCA											970

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CGCAAAAGTC GCGACTACC TCGTGGTGAA GGGCACAACC ACGGAACGGC ATGATCAACA 1030
 TGCTGAGATC ATCGAGGTGC GCTCCGCAGA 1060

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Gly Ala Ala Ala Ala Met Leu Ala Ala Val Leu Leu Leu Thr Pro
 -32 -30 -25 -20
 Ile Thr Val Pro Ala Gly Tyr Pro Gly Ala Val Ala Pro Ala Thr Ala
 -15 -10 -5
 Ala Cys Pro Asp Ala Glu Val Val Phe Ala Arg Gly Arg Phe Glu Pro
 1 5 10 15
 Pro Gly Ile Gly Thr Val Gly Asn Ala Phe Val Ser Ala Leu Arg Ser
 20 25 30
 Lys Val Asn Lys Asn Val Gly Val Tyr Ala Val Lys Tyr Pro Ala Asp
 35 40 45
 Asn Gln Ile Asp Val Gly Ala Asn Asp Met Ser Ala His Ile Gln Ser
 50 55 60
 Met Ala Asn Ser Cys Pro Asn Thr Arg Leu Val Pro Gly Gly Tyr Ser
 65 70 75 80
 Leu Gly Ala Ala Val Thr Asp Val Val Leu Ala Val Pro Thr Gln Met
 85 90 95
 Trp Gly Phe Thr Asn Pro Leu Pro Pro Gly Ser Asp Glu His Ile Ala
 100 105 110
 Ala Val Ala Leu Phe Gly Asn Gly Ser Gln Trp Val Gly Pro Ile Thr
 115 120 125
 Asn Phe Ser Pro Ala Tyr Asn Asp Arg Thr Ile Glu Leu Cys His Gly
 130 135 140
 Asp Asp Pro Val Cys His Pro Ala Asp Pro Asn Thr Trp Glu Ala Asn
 145 150 155 160
 Trp Pro Gln His Leu Ala Gly Ala Tyr Val Ser Ser Gly Met Val Asn
 165 170 175
 Gln Ala Ala Asp Phe Val Ala Gly Lys Leu Gln
 180 185

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 201..998

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 201..998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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CAGATGCTGC GCAACATGTT TCTCGGCGAT CCGGCAGGCA ACACCGATCG AGTGCTTGAC      60
TTTTCCACCG CGGTGACCGG CGGACTGTTC TTCTACCCA CCATCGACTT TCTCGACCAT      120
CCACCGCCCC TACCGCAGGC GCGACGCCA ACTCTGGCAG CCGGGTCGCT ATCGATCGGC      180
AGCTTGAAAG GAAGCCCCCG ATG AAC AAT CTC TAC CGC GAT TTG GCA CCG      230
              Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro
                1             5             10

GTC ACC GAA GCC GCT TGG GCG GAA ATC GAA TTG GAG GCG GCG CGG ACG      278
Val Thr Glu Ala Ala Trp Ala Glu Ile Glu Leu Glu Ala Ala Arg Thr
              15             20             25

TTC AAG CGA CAC ATC GCC GGG CGC CGG GTG GTC GAT GTC AGT GAT CCC      326
Phe Lys Arg His Ile Ala Gly Arg Arg Val Val Asp Val Ser Asp Pro
              30             35             40

GGG GGG CCC GTC ACC GCG GCG GTC AGC ACC GGC CGG CTG ATC GAT GTT      374
Gly Gly Pro Val Thr Ala Ala Val Ser Thr Gly Arg Leu Ile Asp Val
              45             50             55

AAG GCA CCA ACC AAC GGC GTG ATC GCC CAC CTG CGG GCC AGC AAA CCC      422
Lys Ala Pro Thr Asn Gly Val Ile Ala His Leu Arg Ala Ser Lys Pro
              60             65             70

CTT GTC CGG CTA CGG GTT CCG TTT ACC CTG TCG CGC AAC GAG ATC GAC      470
Leu Val Arg Leu Arg Val Pro Phe Thr Leu Ser Arg Asn Glu Ile Asp
              75             80             85             90

GAC GTG GAA CGT GGC TCT AAG GAC TCC GAT TGG GAA CCG GTA AAG GAG      518
Asp Val Glu Arg Gly Ser Lys Asp Ser Asp Trp Glu Pro Val Lys Glu
              95             100             105

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GCG GCC AAG AAG CTG GCC TTC GTC GAG GAC CGC ACA ATA TTC GAA GGC Ala Ala Lys Lys Leu Ala Phe Val Glu Asp Arg Thr Ile Phe Glu Gly 110 115 120	566
TAC AGC GCC GCA TCA ATC GAA GGG ATC CGC AGC GCG AGT TCG AAC CCG Tyr Ser Ala Ala Ser Ile Glu Gly Ile Arg Ser Ala Ser Ser Asn Pro 125 130 135	614
GCG CTG ACG TTG CCC GAG GAT CCC CGT GAA ATC CCT GAT GTC ATC TCC Ala Leu Thr Leu Pro Glu Asp Pro Arg Glu Ile Pro Asp Val Ile Ser 140 145 150	662
CAG GCA TTG TCC GAA CTG CGG TTG GCC GGT GTG GAC GGA CCG TAT TCG Gln Ala Leu Ser Glu Leu Arg Leu Ala Gly Val Asp Gly Pro Tyr Ser 155 160 165 170	710
GTG TTG CTC TCT GCT GAC GTC TAC ACC AAG GTT AGC GAG ACT TCC GAT Val Leu Leu Ser Ala Asp Val Tyr Thr Lys Val Ser Glu Thr Ser Asp 175 180 185	758
CAC GGC TAT CCC ATC CGT GAG CAT CTG AAC CGG CTG GTG GAC GGG GAC His Gly Tyr Pro Ile Arg Glu His Leu Asn Arg Leu Val Asp Gly Asp 190 195 200	806
ATC ATT TGG GCC CCG GCC ATC GAC GGC GCG TTC GTG CTG ACC ACT CGA Ile Ile Trp Ala Pro Ala Ile Asp Gly Ala Phe Val Leu Thr Thr Arg 205 210 215	854
GGC GGC GAC TTC GAC CTA CAG CTG GGC ACC GAC GTT GCA ATC GGG TAC Gly Gly Asp Phe Asp Leu Gln Leu Gly Thr Asp Val Ala Ile Gly Tyr 220 225 230	902
GCC AGC CAC GAC ACG GAC ACC GAG CGC CTC TAC CTG CAG GAG ACG CTG Ala Ser His Asp Thr Asp Thr Glu Arg Leu Tyr Leu Gln Glu Thr Leu 235 240 245 250	950
ACG TTC CTT TGC TAC ACC GCC GAG GCG TCG GTC GCG CTC AGC CAC TAA Thr Phe Leu Cys Tyr Thr Ala Glu Ala Ser Val Ala Leu Ser His 255 260 265	998
GGCACGAGCG CGAGCAATAG CTCCTATGGC AAGCGGCCCGC GGGTTGGGTG TGTTCCGAGC	1058
TGGGCTGGTG GACGGTGCGC AGGGCCTGGA AGACGGTGCG GGCTAGGCGG CGTTTGAGGC	1118
AGCGTAGTGC TGC GCGTTTG GTTTTCCCGG CGTCTTG CAG CCTTTGGTAG TAGGCCTGGC	1178
CCCGGCTGTC GGTCATCCGG	1198

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro Val Thr Glu Ala Ala Trp
 1 5 10 15
 Ala Glu Ile Glu Leu Glu Ala Ala Arg Thr Phe Lys Arg His Ile Ala
 20 25 30
 Gly Arg Arg Val Val Asp Val Ser Asp Pro Gly Gly Pro Val Thr Ala
 35 40 45
 Ala Val Ser Thr Gly Arg Leu Ile Asp Val Lys Ala Pro Thr Asn Gly
 50 55 60
 Val Ile Ala His Leu Arg Ala Ser Lys Pro Leu Val Arg Leu Arg Val
 65 70 75 80
 Pro Phe Thr Leu Ser Arg Asn Glu Ile Asp Asp Val Glu Arg Gly Ser
 85 90 95
 Lys Asp Ser Asp Trp Glu Pro Val Lys Glu Ala Ala Lys Lys Leu Ala
 100 105 110
 Phe Val Glu Asp Arg Thr Ile Phe Glu Gly Tyr Ser Ala Ala Ser Ile
 115 120 125
 Glu Gly Ile Arg Ser Ala Ser Ser Asn Pro Ala Leu Thr Leu Pro Glu
 130 135 140
 Asp Pro Arg Glu Ile Pro Asp Val Ile Ser Gln Ala Leu Ser Glu Leu
 145 150 155 160
 Arg Leu Ala Gly Val Asp Gly Pro Tyr Ser Val Leu Leu Ser Ala Asp
 165 170 175
 Val Tyr Thr Lys Val Ser Glu Thr Ser Asp His Gly Tyr Pro Ile Arg
 180 185 190
 Glu His Leu Asn Arg Leu Val Asp Gly Asp Ile Ile Trp Ala Pro Ala
 195 200 205
 Ile Asp Gly Ala Phe Val Leu Thr Thr Arg Gly Gly Asp Phe Asp Leu
 210 215 220
 Gln Leu Gly Thr Asp Val Ala Ile Gly Tyr Ala Ser His Asp Thr Asp
 225 230 235 240
 Thr Glu Arg Leu Tyr Leu Gln Glu Thr Leu Thr Phe Leu Cys Tyr Thr
 245 250 255
 Ala Glu Ala Ser Val Ala Leu Ser His
 260 265

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 1
- (D) OTHER INFORMATION: Ala is Ala or Ser

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 13
- (D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala	Glu	Leu	Asp	Ala	Pro	Ala	Gln	Ala	Gly	Thr	Glu	Xaa	Ala	Val
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Ala	Gln	Ile	Thr	Leu	Arg	Gly	Asn	Ala	Ile	Asn	Thr	Val	Gly	Glu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Thr	Asn	Ser	Pro	Leu	Ala	Thr	Ala	Thr	Ala	Thr	Leu	His	Thr	Asn
1				5				10						15

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(B) STRAIN: H37Rv

(ix) Feature:

(A) NAME/KEY: Other

(B) LOCATION: 2

143

(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Ala	Xaa	Pro	Asp	Ala	Glu	Val	Val	Phe	Ala	Arg	Gly	Arg	Phe	Glu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 1
- (C) OTHER INFORMATION: Xaa is unknown

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 2
- (D) OTHER INFORMATION: Ile is Ile or Val

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 10
- (D) OTHER INFORMATION: Val is Val or Thr

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 11
- (D) OTHER INFORMATION: Val is Val or Phe

(ix) FEATURE:

- (A) NAME/KEY: Duplication
- (B) LOCATION: 14
- (D) OTHER INFORMATION: Asp is Asp or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Xaa	Ile	Gln	Lys	Ser	Leu	Glu	Leu	Ile	Val	Val	Thr	Ala	Asp	Glu
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

144

- (A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
(B) STRAIN: H37Rv

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Asn Asn Leu Tyr Arg Asp Leu Ala Pro Val Thr Glu Ala Ala Trp
1 5 10 15

Ala Glu Ile

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCCGGCTCGA GAACCTSTAC CGCGACCTSG CSCC

34

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GGGCCGGATC CGASGCSGCG TCCTTTSACSG GYTGCCA

37

(2) INFORMATION FOR SEQ ID NO: 26:

145

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GGAAGCCCCA TATGAACAAT CTCTACCG

28

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CGCGCTCAGC CCTTAGTGAC TGAGCGCGAC CG

32

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CTCGAATTCG CCGGGTGCAC ACAG

24

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

146

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CTCGAATTCG CCCCATACG AGAAC

25

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GTGTATCTGC TGGAC

15

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCGACTGGCT GGCCG

15

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

147

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGGAATTCTG CTTAGCGGAT CGCA

24

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CCCACATTCC GTTGG

15

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GTCCAGCAGA TACAC

15

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GTACGAGAAT TCATGTCGCA AATCATG

27

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GTACGAGAAT TCGAGCTTGG GGTGCCG

27

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CGATTCCAAG CTTGTGGCCG CCGACCCG

28

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CGTTAGGGAT CCTCATCGCC ATGGTGTGG

30

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CGTTAGGGAT CCGGTTCCAC TGTGCC

26

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGTTAGGGAT CCTCAGGTCT TTTCGATG

28

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 952 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis
- (B) STRAIN: H37Rv

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 45..944

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..143

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 144..941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAATTGCGCCG GGTGCACACA GCCTTACACG ACGGAGGTGG ACAC ATG AAG GGT CGG	56
Met Lys Gly Arg	
-33 -30	
TCG GCG CTG CTG CGG GCG CTC TGG ATT GCC GCA CTG TCA TTC GGG TTG	104
Ser Ala Leu Leu Arg Ala Leu Trp Ile Ala Ala Leu Ser Phe Gly Leu	
-25 -20 -15	
GGC GGT GTC GCG GTA GCC GCG GAA CCC ACC GCC AAG GCC GCC CCA TAC	152
Gly Gly Val Ala Val Ala Ala Glu Pro Thr Ala Lys Ala Ala Pro Tyr	
-10 -5 1	
GAG AAC CTG ATG GTG CCG TCG CCC TCG ATG GGC CGG GAC ATC CCG GTG	200
Glu Asn Leu Met Val Pro Ser Pro Ser Met Gly Arg Asp Ile Pro Val	
5 10 15	
GCC TTC CTA GCC GGT GGG CCG CAC GCG GTG TAT CTG CTG GAC GCC TTC	248
Ala Phe Leu Ala Gly Gly Pro His Ala Val Tyr Leu Leu Asp Ala Phe	
20 25 30 35	
AAC GCC GGC CCG GAT GTC AGT AAC TGG GTC ACC GCG GGT AAC GCG ATG	296
Asn Ala Gly Pro Asp Val Ser Asn Trp Val Thr Ala Gly Asn Ala Met	
40 45 50	
AAC ACG TTG GCG GGC AAG GGG ATT TCG GTG GTG GCA CCG GCC GGT GGT	344
Asn Thr Leu Ala Gly Lys Gly Ile Ser Val Val Ala Pro Ala Gly Gly	
55 60 65	
GCG TAC AGC ATG TAC ACC AAC TGG GAG CAG GAT GGC AGC AAG CAG TGG	392
Ala Tyr Ser Met Tyr Thr Asn Trp Glu Gln Asp Gly Ser Lys Gln Trp	
70 75 80	
GAC ACC TTC TTG TCC GCT GAG CTG CCC GAC TGG CTG GCC GCT AAC CGG	440
Asp Thr Phe Leu Ser Ala Glu Leu Pro Asp Trp Leu Ala Ala Asn Arg	
85 90 95	
GGC TTG GCC CCC GGT GGC CAT GCG GCC GTT GGC GCC GCT CAG GGC GGT	488
Gly Leu Ala Pro Gly Gly His Ala Ala Val Gly Ala Ala Gln Gly Gly	
100 105 110 115	
TAC GGG GCG ATG GCG CTG GCG GCC TTC CAC CCC GAC CGC TTC GGC TTC	536
Tyr Gly Ala Met Ala Leu Ala Ala Phe His Pro Asp Arg Phe Gly Phe	
120 125 130	

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GCT GGC TCG ATG TCG GGC TTT TTG TAC CCG TCG AAC ACC ACC ACC AAC	584
Ala Gly Ser Met Ser Gly Phe Leu Tyr Pro Ser Asn Thr Thr Thr Asn	
135 140 145	
GGT GCG ATC GCG GCG GGC ATG CAG CAA TTC GGC GGT GTG GAC ACC AAC	632
Gly Ala Ile Ala Ala Gly Met Gln Gln Phe Gly Gly Val Asp Thr Asn	
150 155 160	
GGA ATG TGG GGA GCA CCA CAG CTG GGT CGG TGG AAG TGG CAC GAC CCG	680
Gly Met Trp Gly Ala Pro Gln Leu Gly Arg Trp Lys Trp His Asp Pro	
165 170 175	
TGG GTG CAT GCC AGC CTG CTG GCG CAA AAC AAC ACC CGG GTG TGG GTG	728
Trp Val His Ala Ser Leu Leu Ala Gln Asn Asn Thr Arg Val Trp Val	
180 185 190 195	
TGG AGC CCG ACC AAC CCG GGA GCC AGC GAT CCC GCC GCC ATG ATC GGC	776
Trp Ser Pro Thr Asn Pro Gly Ala Ser Asp Pro Ala Ala Met Ile Gly	
200 205 210	
CAA ACC GCC GAG GCG ATG GGT AAC AGC CGC ATG TTC TAC AAC CAG TAT	824
Gln Thr Ala Glu Ala Met Gly Asn Ser Arg Met Phe Tyr Asn Gln Tyr	
215 220 225	
CGC AGC GTC GGC GGG CAC AAC GGA CAC TTC GAC TTC CCA GCC AGC GGT	872
Arg Ser Val Gly Gly His Asn Gly His Phe Asp Phe Pro Ala Ser Gly	
230 235 240	
GAC AAC GGC TGG GGC TCG TGG GCG CCC CAG CTG GGC GCT ATG TCG GGC	920
Asp Asn Gly Trp Gly Ser Trp Ala Pro Gln Leu Gly Ala Met Ser Gly	
245 250 255	
GAT ATC GTC GGT GCG ATC CGC TAA GCGAATTC	952
Asp Ile Val Gly Ala Ile Arg	
260 265	

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Lys Gly Arg Ser Ala Leu Leu Arg Ala Leu Trp Ile Ala Ala Leu	
-33 -30 -25 -20	
Ser Phe Gly Leu Gly Gly Val Ala Val Ala Ala Glu Pro Thr Ala Lys	
-15 -10 -5	
Ala Ala Pro Tyr Glu Asn Leu Met Val Pro Ser Pro Ser Met Gly Arg	
1 5 10 15	
Asp Ile Pro Val Ala Phe Leu Ala Gly Gly Pro His Ala Val Tyr Leu	
20 25 30	

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Leu Asp Ala Phe Asn Ala Gly Pro Asp Val Ser Asn Trp Val Thr Ala
      35                      40                      45

Gly Asn Ala Met Asn Thr Leu Ala Gly Lys Gly Ile Ser Val Val Ala
      50                      55                      60

Pro Ala Gly Gly Ala Tyr Ser Met Tyr Thr Asn Trp Glu Gln Asp Gly
      65                      70                      75

Ser Lys Gln Trp Asp Thr Phe Leu Ser Ala Glu Leu Pro Asp Trp Leu
      80                      85                      90                      95

Ala Ala Asn Arg Gly Leu Ala Pro Gly Gly His Ala Ala Val Gly Ala
      100                     105                     110

Ala Gln Gly Gly Tyr Gly Ala Met Ala Leu Ala Ala Phe His Pro Asp
      115                     120                     125

Arg Phe Gly Phe Ala Gly Ser Met Ser Gly Phe Leu Tyr Pro Ser Asn
      130                     135                     140

Thr Thr Thr Asn Gly Ala Ile Ala Ala Gly Met Gln Gln Phe Gly Gly
      145                     150                     155

Val Asp Thr Asn Gly Met Trp Gly Ala Pro Gln Leu Gly Arg Trp Lys
      160                     165                     170                     175

Trp His Asp Pro Trp Val His Ala Ser Leu Leu Ala Gln Asn Asn Thr
      180                     185                     190

Arg Val Trp Val Trp Ser Pro Thr Asn Pro Gly Ala Ser Asp Pro Ala
      195                     200                     205

Ala Met Ile Gly Gln Thr Ala Glu Ala Met Gly Asn Ser Arg Met Phe
      210                     215                     220

Tyr Asn Gln Tyr Arg Ser Val Gly Gly His Asn Gly His Phe Asp Phe
      225                     230                     235

Pro Ala Ser Gly Asp Asn Gly Trp Gly Ser Trp Ala Pro Gln Leu Gly
      240                     245                     250                     255

Ala Met Ser Gly Asp Ile Val Gly Ala Ile Arg
      260                     265

```

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GCAACACCCG GGATGTCGCA AATCATG

27

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTAACACCCG GGGTGGCCGC CGACCCG

27

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

CTACTAAGCT TGGATCCCTA GCCGCCCAT TTGGCGG

37

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

CTACTAAGCT TCCATGGTCA GGTCTTTTCG ATGCTTAC

38

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 105...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTGCCGCGCT CCCAGGGTT CTTATGGTTC GATATACCTG AGTTTGATGG AAGTCCGATG	60
ACCAGCAGTC AGCATACGGC ATGGCCGAAA AGAGTGGGGT GATG ATG GCC GAG GAT	116
Met Ala Glu Asp	
1	
GTT CGC GCC GAG ATC GTG GCC AGC GTT CTC GAA GTC GTT GTC AAC GAA	164
Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val Val Asn Glu	
5 10 15 20	
GGC GAT CAG ATC GAC AAG GGC GAC GTC GTG GTG CTG CTG GAG TCG ATG	212
Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu Glu Ser Met	
25 30 35	
AAG ATG GAG ATC CCC GTC CTG GCC GAA GCT GCC GGA ACG GTC AGC AAG	260
Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr Val Ser Lys	
40 45 50	
GTG GCG GTA TCG GTG GGC GAT GTC ATT CAG GCC GGC GAC CTT ATC GCG	308
Val Ala Val Ser Val Gly Asp Val Ile Gln Ala Gly Asp Leu Ile Ala	
55 60 65	
GTG ATC AGC TAGTCGTTGA TAGTCACTCA TGTCCACACT CGGTGATCTG CTCGCCGAA	366
Val Ile Ser	
70	
CACACGGTGC TGCCGGGGCAG CGCGGTGGAC CACCTGCATG CGGTGGTCCG GGAGTGGCAG	426
CTCCTTGCCG ACTTGTCGTT TGCC	450

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

155

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

Met Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val
 1             5             10             15
Val Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu
             20             25             30
Leu Glu Ser Met Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly
             35             40             45
Thr Val Ser Lys Val Ala Val Ser Val Gly Asp Val Ile Gln Ala Gly
             50             55             60
Asp Leu Ile Ala Val Ile Ser
65             70

```

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 113...640

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

GGGTACCCAT CGATGGGTTG CGGTTCCGGCA CCGAGGTGCT AACGCACTTG CTGACACACT      60
GCTAGTCGAA AACGAGGCTA GTCGCAACGT CGATCACACG AGAGGACTGA CC ATG ACA      118
                               Met Thr
                               1
ACT TCA CCC GAC CCG TAT GCC GCG CTG CCC AAG CTG CCG TCC TTC AGC      166
Thr Ser Pro Asp Pro Tyr Ala Ala Leu Pro Lys Leu Pro Ser Phe Ser
             5             10             15
CTG ACG TCA ACC TCG ATC ACC GAT GGG CAG CCG CTG GCT ACA CCC CAG      214
Leu Thr Ser Thr Ser Ile Thr Asp Gly Gln Pro Leu Ala Thr Pro Gln
             20             25             30
GTC AGC GGG ATC ATG GGT GCG GGC GGG GCG GAT GCC AGT CCG CAG CTG      262
Val Ser Gly Ile Met Gly Ala Gly Gly Ala Asp Ala Ser Pro Gln Leu
             35             40             45             50

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AGG TGG TCG GGA TTT CCC AGC GAG ACC CGC AGC TTC GCG GTA ACC GTC      310
Arg Trp Ser Gly Phe Pro Ser Glu Thr Arg Ser Phe Ala Val Thr Val
                    55                                60                                65

TAC GAC CCT GAT GCC CCC ACC CTG TCC GGG TTC TGG CAC TGG GCG GTG      358
Tyr Asp Pro Asp Ala Pro Thr Leu Ser Gly Phe Trp His Trp Ala Val
                    70                                75                                80

GCC AAC CTG CCT GCC AAC GTC ACC GAG TTG CCC GAG GGT GTC GGC GAT      406
Ala Asn Leu Pro Ala Asn Val Thr Glu Leu Pro Glu Gly Val Gly Asp
                    85                                90                                95

GGC CGC GAA CTG CCG GGC GGG GCA CTG ACA TTG GTC AAC GAC GCC GGT      454
Gly Arg Glu Leu Pro Gly Gly Ala Leu Thr Leu Val Asn Asp Ala Gly
                    100                               105                               110

ATG CGC CGG TAT GTG GGT GCG GCG CCG CCT CCC GGT CAT GGG GTG CAT      502
Met Arg Arg Tyr Val Gly Ala Ala Pro Pro Pro Gly His Gly Val His
                    115                               120                               125                               130

CGC TAC TAC GTC GCG GTA CAC GCG GTG AAG GTC GAA AAG CTC GAC CTC      550
Arg Tyr Tyr Val Ala Val His Ala Val Lys Val Glu Lys Leu Asp Leu
                    135                               140                               145

CCC GAG GAC GCG AGT CCT GCA TAT CTG GGA TTC AAC CTG TTC CAG CAC      598
Pro Glu Asp Ala Ser Pro Ala Tyr Leu Gly Phe Asn Leu Phe Gln His
                    150                               155                               160

GCG ATT GCA CGA GCG GTC ATC TTC GGC ACC TAC GAG CAG CGT TAGCGCTTT      649
Ala Ile Ala Arg Ala Val Ile Phe Gly Thr Tyr Glu Gln Arg
                    165                               170                               175

AGCTGGGTTG CCGACGTCTT GCCGAGCCGA CCGCTTCGTG CAGCGAGCCG AACCCGCCGT      709

CATGCAGCCT GCGGGCAATG CCTTCATGGA TGTCTTGGC C      750

```

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

Met Thr Thr Ser Pro Asp Pro Tyr Ala Ala Leu Pro Lys Leu Pro Ser
 1                               5                               10                               15

Phe Ser Leu Thr Ser Thr Ser Ile Thr Asp Gly Gln Pro Leu Ala Thr
                    20                               25                               30

Pro Gln Val Ser Gly Ile Met Gly Ala Gly Gly Ala Asp Ala Ser Pro
                    35                               40                               45

```

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Gln Leu Arg Trp Ser Gly Phe Pro Ser Glu Thr Arg Ser Phe Ala Val
 50 55 60

Thr Val Tyr Asp Pro Asp Ala Pro Thr Leu Ser Gly Phe Trp His Trp
 65 70 75 80

Ala Val Ala Asn Leu Pro Ala Asn Val Thr Glu Leu Pro Glu Gly Val
 85 90 95

Gly Asp Gly Arg Glu Leu Pro Gly Gly Ala Leu Thr Leu Val Asn Asp
 100 105 110

Ala Gly Met Arg Arg Tyr Val Gly Ala Ala Pro Pro Pro Gly His Gly
 115 120 125

Val His Arg Tyr Tyr Val Ala Val His Ala Val Lys Val Glu Lys Leu
 130 135 140

Asp Leu Pro Glu Asp Ala Ser Pro Ala Tyr Leu Gly Phe Asn Leu Phe
 145 150 155 160

Gln His Ala Ile Ala Arg Ala Val Ile Phe Gly Thr Tyr Glu Gln Arg
 165 170 175

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 18...695
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 18...134
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

TCATGAGGTT CATCGGG GTG ATC CCA CGC CCG CAG CCG CAT TCG GGC CGC 50
 Met Ile Pro Arg Pro Gln Pro His Ser Gly Arg
 -35 -30

TGG CGA GCC GGT GCC GCA CGC CGC CTC ACC AGC CTG GTG GCC GCC GCC 98
 Trp Arg Ala Gly Ala Ala Arg Arg Leu Thr Ser Leu Val Ala Ala Ala
 -25 -20 -15

TTT GCG GCG GCC ACA CTG TTG CTT ACC CCC GCG CTG GCA CCA CCG GCA 146
 Phe Ala Ala Ala Thr Leu Leu Thr Pro Ala Leu Ala Pro Pro Ala
 -10 -5 1 5

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TCG GCG GGC TGC CCG GAT GCC GAG GTG GTG TTC GCC CGC GGA ACC GGC	194
Ser Ala Gly Cys Pro Asp Ala Glu Val Val Phe Ala Arg Gly Thr Gly	
10 15 20	
GAA CCA CCT GGC CTC GGT CGG GTA GGC CAA GCT TTC GTC AGT TCA TTG	242
Glu Pro Pro Gly Leu Gly Arg Val Gly Gln Ala Phe Val Ser Ser Leu	
25 30 35	
CGC CAG CAG ACC AAC AAG AGC ATC GGG ACA TAC GGA GTC AAC TAC CCG	290
Arg Gln Gln Thr Asn Lys Ser Ile Gly Thr Tyr Gly Val Asn Tyr Pro	
40 45 50	
GCC AAC GGT GAT TTC TTG GCC GCC GCT GAC GGC GCG AAC GAC GCC AGC	338
Ala Asn Gly Asp Phe Leu Ala Ala Ala Asp Gly Ala Asn Asp Ala Ser	
55 60 65	
GAC CAC ATT CAG CAG ATG GCC AGC GCG TGC CGG GCC ACG AGG TTG GTG	386
Asp His Ile Gln Gln Met Ala Ser Ala Cys Arg Ala Thr Arg Leu Val	
70 75 80 85	
CTC GGC GGC TAC TCC CAG GGT GCG GCC GTG ATC GAC ATC GTC ACC GCC	434
Leu Gly Gly Tyr Ser Gln Gly Ala Ala Val Ile Asp Ile Val Thr Ala	
90 95 100	
GCA CCA CTG CCC GGC CTC GGG TTC ACG CAG CCG TTG CCG CCC GCA GCG	482
Ala Pro Leu Pro Gly Leu Gly Phe Thr Gln Pro Leu Pro Pro Ala Ala	
105 110 115	
GAC GAT CAC ATC GCC GCG ATC GCC CTG TTC GGG AAT CCC TCG GGC CGC	530
Asp Asp His Ile Ala Ala Ile Ala Leu Phe Gly Asn Pro Ser Gly Arg	
120 125 130	
GCT GGC GGG CTG ATG AGC GCC CTG ACC CCT CAA TTC GGG TCC AAG ACC	578
Ala Gly Gly Leu Met Ser Ala Leu Thr Pro Gln Phe Gly Ser Lys Thr	
135 140 145	
ATC AAC CTC TGC AAC AAC GGC GAC CCG ATT TGT TCG GAC GGC AAC CGG	626
Ile Asn Leu Cys Asn Asn Gly Asp Pro Ile Cys Ser Asp Gly Asn Arg	
150 155 160 165	
TGG CGA GCG CAC CTA GGC TAC GTG CCC GGG ATG ACC AAC CAG GCG GCG	674
Trp Arg Ala His Leu Gly Tyr Val Pro Gly Met Thr Asn Gln Ala Ala	
170 175 180	
CGT TTC GTC GCG AGC AGG ATC TAACGCGAGC CGCCCCATAG ATTCCGGCTA AGCA	729
Arg Phe Val Ala Ser Arg Ile	
185	
ACGGCTGCGC CGCCGCCCGG CCACGAGTGA CCGCCGCCGA CTGGCACACC GCTTACCACG	789
GCCTTATGCT G	800

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal
(ix) FEATURE:

(A) NAME/KEY: Signal Sequence
(B) LOCATION: 1...38
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

Met Ile Pro Arg Pro Gln Pro His Ser Gly Arg Trp Arg Ala Gly Ala
      -35                      -30                      -25

Ala Arg Arg Leu Thr Ser Leu Val Ala Ala Ala Phe Ala Ala Ala Thr
      -20                      -15                      -10

Leu Leu Leu Thr Pro Ala Leu Ala Pro Pro Ala Ser Ala Gly Cys Pro
      -5                      1                      5                      10

Asp Ala Glu Val Val Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Leu
      15                      20                      25

Gly Arg Val Gly Gln Ala Phe Val Ser Ser Leu Arg Gln Gln Thr Asn
      30                      35                      40

Lys Ser Ile Gly Thr Tyr Gly Val Asn Tyr Pro Ala Asn Gly Asp Phe
      45                      50                      55

Leu Ala Ala Ala Asp Gly Ala Asn Asp Ala Ser Asp His Ile Gln Gln
      60                      65                      70

Met Ala Ser Ala Cys Arg Ala Thr Arg Leu Val Leu Gly Gly Tyr Ser
      75                      80                      85                      90

Gln Gly Ala Ala Val Ile Asp Ile Val Thr Ala Ala Pro Leu Pro Gly
      95                      100                      105

Leu Gly Phe Thr Gln Pro Leu Pro Pro Ala Ala Asp Asp His Ile Ala
      110                      115                      120

Ala Ile Ala Leu Phe Gly Asn Pro Ser Gly Arg Ala Gly Gly Leu Met
      125                      130                      135

Ser Ala Leu Thr Pro Gln Phe Gly Ser Lys Thr Ile Asn Leu Cys Asn
      140                      145                      150

Asn Gly Asp Pro Ile Cys Ser Asp Gly Asn Arg Trp Arg Ala His Leu
      155                      160                      165                      170

Gly Tyr Val Pro Gly Met Thr Asn Gln Ala Ala Arg Phe Val Ala Ser
      175                      180                      185

Arg Ile

```

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 73...615
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

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CTAGGAAAGC CTTTCCTGAG TAAGTATTGC CTTCGTTGCA TACCGCCCTT TACCTGCGTT      60
AATCTGCATT TT ATG ACA GAA TAC GAA GGG CCT AAG ACA AAA TTC CAC GCG      111
      Met Thr Glu Tyr Glu Gly Pro Lys Thr Lys Phe His Ala
           1             5             10
TTA ATG CAG GAA CAG ATT CAT AAC GAA TTC ACA GCG GCA CAA CAA TAT      159
Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr Ala Ala Gln Gln Tyr
      15             20             25
GTC GCG ATC GCG GTT TAT TTC GAC AGC GAA GAC CTG CCG CAG TTG GCG      207
Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp Leu Pro Gln Leu Ala
      30             35             40             45
AAG CAT TTT TAC AGC CAA GCG GTC GAG GAA CGA AAC CAT GCA ATG ATG      255
Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg Asn His Ala Met Met
           50             55             60
CTC GTG CAA CAC CTG CTC GAC CGC GAC CTT CGT GTC GAA ATT CCC GGC      303
Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg Val Glu Ile Pro Gly
           65             70             75
GTA GAC ACG GTG CGA AAC CAG TTC GAC AGA CCC CGC GAG GCA CTG GCG      351
Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro Arg Glu Ala Leu Ala
           80             85             90
CTG GCG CTC GAT CAG GAA CGC ACA GTC ACC GAC CAG GTC GGT CGG CTG      399
Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp Gln Val Gly Arg Leu
           95             100             105
ACA GCG GTG GCC CGC GAC GAG GGC GAT TTC CTC GGC GAG CAG TTC ATG      447
Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu Gly Glu Gln Phe Met
      110             115             120             125
CAG TGG TTC TTG CAG GAA CAG ATC GAA GAG GTG GCC TTG ATG GCA ACC      495
Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val Ala Leu Met Ala Thr
           130             135             140
CTG GTG CGG GTT GCC GAT CGG GCC GGG GCC AAC CTG TTC GAG CTA GAG      543
Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn Leu Phe Glu Leu Glu
           145             150             155

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AAC TTC GTC GCA CGT GAA GTG GAT GTG GCG CCG GCC GCA TCA GGC GCC 591
 Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro Ala Ala Ser Gly Ala
 160 170

CCG CAC GCT GCC GGG GGC CGC CTC TAGATCCCTG GCGGGGATCA GCGAGTGGTC 645
 Pro His Ala Ala Gly Gly Arg Leu
 175 180

CCGTTTCGCCC GCCCGTCTTC CAGCCAGGCC TTGGTGCGGC CGGGGTGGTG AGTAC 700

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met Thr Glu Tyr Glu Gly Pro Lys Thr Lys Phe His Ala Leu Met Gln
 1 10 15

Glu Gln Ile His Asn Glu Phe Thr Ala Ala Gln Gln Tyr Val Ala Ile
 20 25 30

Ala Val Tyr Phe Asp Ser Glu Asp Leu Pro Gln Leu Ala Lys His Phe
 35 40 45

Tyr Ser Gln Ala Val Glu Glu Arg Asn His Ala Met Met Leu Val Gln
 50 55 60

His Leu Leu Asp Arg Asp Leu Arg Val Glu Ile Pro Gly Val Asp Thr
 65 70 75 80

Val Arg Asn Gln Phe Asp Arg Pro Arg Glu Ala Leu Ala Leu Ala Leu
 85 90 95

Asp Gln Glu Arg Thr Val Thr Asp Gln Val Gly Arg Leu Thr Ala Val
 100 105 110

Ala Arg Asp Glu Gly Asp Phe Leu Gly Glu Gln Phe Met Gln Trp Phe
 115 120 125

Leu Gln Glu Gln Ile Glu Glu Val Ala Leu Met Ala Thr Leu Val Arg
 130 135 140

Val Ala Asp Arg Ala Gly Ala Asn Leu Phe Glu Leu Glu Asn Phe Val
 145 150 155 160

Ala Arg Glu Val Asp Val Ala Pro Ala Ala Ser Gly Ala Pro His Ala
 165 170 175

Ala Gly Gly Arg Leu
180

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 950 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 133...918
 (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
 (B) LOCATION: 133...233
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TGGGCTCGGC ACTGGCTCTC CCACGGTGGC GCGCTGATTT CTCCCCACGG TAGGCGTTGC	60
GACGCATGTT CTTACCGTC TATCCACAGC TACCGACATT TGCTCCGGCT GGATCGCGGG	120
TAAAATTCCG TC GTG AAC AAT CGA CCC ATC CGC CTG CTG ACA TCC GGC AGG	171
Met Asn Asn Arg Pro Ile Arg Leu Leu Thr Ser Gly Arg	
-30 -25	
GCT GGT TTG GGT GCG GGC GCA TTG ATC ACC GCC GTC GTC CTG CTC ATC	219
Ala Gly Leu Gly Ala Gly Ala Leu Ile Thr Ala Val Val Leu Leu Ile	
-20 -15 -10 -5	
GCC TTG GGC GCT GTT TGG ACC CCG GTT GCC TTC GCC GAT GGA TGC CCG	267
Ala Leu Gly Ala Val Trp Thr Pro Val Ala Phe Ala Asp Gly Cys Pro	
1 5 10	
GAC GCC GAA GTC ACG TTC GCC CGC GGC ACC GGC GAG CCG CCC GGA ATC	315
Asp Ala Glu Val Thr Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Ile	
15 20 25	
GGG CGC GTT GGC CAG GCG TTC GTC GAC TCG CTG CGC CAG CAG ACT GGC	363
Gly Arg Val Gly Gln Ala Phe Val Asp Ser Leu Arg Gln Gln Thr Gly	
30 35 40	
ATG GAG ATC GGA GTA TAC CCG GTG AAT TAC GCC GCC AGC CGC CTA CAG	411
Met Glu Ile Gly Val Tyr Pro Val Asn Tyr Ala Ala Ser Arg Leu Gln	
45 50 55 60	
CTG CAC GGG GGA GAC GGC GCC AAC GAC GCC ATA TCG CAC ATT AAG TCC	459
Leu His Gly Gly Asp Gly Ala Asn Asp Ala Ile Ser His Ile Lys Ser	
65 70 75	

163

ATG GCC TCG TCA TGC CCG AAC ACC AAG CTG GTC TTG GGC GGC TAT TCG	507
Met Ala Ser Ser Cys Pro Asn Thr Lys Leu Val Leu Gly Gly Tyr Ser	
80 85 90	
CAG GGC GCA ACC GTG ATC GAT ATC GTG GCC GGG GTT CCG TTG GGC AGC	555
Gln Gly Ala Thr Val Ile Asp Ile Val Ala Gly Val Pro Leu Gly Ser	
95 100 105	
ATC AGC TTT GGC AGT CCG CTA CCT GCG GCA TAC GCA GAC AAC GTC GCA	603
Ile Ser Phe Gly Ser Pro Leu Pro Ala Ala Tyr Ala Asp Asn Val Ala	
110 115 120	
GCG GTC GCG GTC TTC GGC AAT CCG TCC AAC CGC GCC GGC GGA TCG CTG	651
Ala Val Ala Val Phe Gly Asn Pro Ser Asn Arg Ala Gly Gly Ser Leu	
125 130 135 140	
TCG AGC CTG AGC CCG CTA TTC GGT TCC AAG GCG ATT GAC CTG TGC AAT	699
Ser Ser Leu Ser Pro Leu Phe Gly Ser Lys Ala Ile Asp Leu Cys Asn	
145 150 155	
CCC ACC GAT CCG ATC TGC CAT GTG GGC CCC GGC AAC GAA TTC AGC GGA	747
Pro Thr Asp Pro Ile Cys His Val Gly Pro Gly Asn Glu Phe Ser Gly	
160 165 170	
CAC ATC GAC GGC TAC ATA CCC ACC TAC ACC ACC CAG GCG GCT AGT TTC	795
His Ile Asp Gly Tyr Ile Pro Thr Tyr Thr Thr Gln Ala Ala Ser Phe	
175 180 185	
GTC GTG CAG AGG CTC CGC GCC GGG TCG GTG CCA CAT CTG CCT GGA TCC	843
Val Val Gln Arg Leu Arg Ala Gly Ser Val Pro His Leu Pro Gly Ser	
190 195 200	
GTC CCG CAG CTG CCC GGG TCT GTC CTT CAG ATG CCC GGC ACT GCC GCA	891
Val Pro Gln Leu Pro Gly Ser Val Leu Gln Met Pro Gly Thr Ala Ala	
205 210 215 220	
CCG GCT CCC GAA TCG CTG CAC GGT CGC TGACGCTTTG TCAGTAAGCC CATAAAA	945
Pro Ala Pro Glu Ser Leu His Gly Arg	
225	
TCGCG	950

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...33

164

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

Met Asn Asn Arg Pro Ile Arg Leu Leu Thr Ser Gly Arg Ala Gly Leu
 -30 -25 -20

Gly Ala Gly Ala Leu Ile Thr Ala Val Val Leu Leu Ile Ala Leu Gly
 -15 -10 -5

Ala Val Trp Thr Pro Val Ala Phe Ala Asp Gly Cys Pro Asp Ala Glu
 1 5 10 15

Val Thr Phe Ala Arg Gly Thr Gly Glu Pro Pro Gly Ile Gly Arg Val
 20 25 30

Gly Gln Ala Phe Val Asp Ser Leu Arg Gln Gln Thr Gly Met Glu Ile
 35 40 45

Gly Val Tyr Pro Val Asn Tyr Ala Ala Ser Arg Leu Gln Leu His Gly
 50 55 60

Gly Asp Gly Ala Asn Asp Ala Ile Ser His Ile Lys Ser Met Ala Ser
 65 70 75

Ser Cys Pro Asn Thr Lys Leu Val Leu Gly Gly Tyr Ser Gln Gly Ala
 80 85 90 95

Thr Val Ile Asp Ile Val Ala Gly Val Pro Leu Gly Ser Ile Ser Phe
 100 105 110

Gly Ser Pro Leu Pro Ala Ala Tyr Ala Asp Asn Val Ala Ala Val Ala
 115 120 125

Val Phe Gly Asn Pro Ser Asn Arg Ala Gly Gly Ser Leu Ser Ser Leu
 130 135 140

Ser Pro Leu Phe Gly Ser Lys Ala Ile Asp Leu Cys Asn Pro Thr Asp
 145 150 155

Pro Ile Cys His Val Gly Pro Gly Asn Glu Phe Ser Gly His Ile Asp
 160 165 170 175

Gly Tyr Ile Pro Thr Tyr Thr Thr Gln Ala Ala Ser Phe Val Val Gln
 180 185 190

Arg Leu Arg Ala Gly Ser Val Pro His Leu Pro Gly Ser Val Pro Gln
 195 200 205

Leu Pro Gly Ser Val Leu Gln Met Pro Gly Thr Ala Ala Pro Ala Pro
 210 215 220

Glu Ser Leu His Gly Arg
 225

(2) INFORMATION FOR SEQ ID NO: 57:

165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 94...966
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 94...264
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CGAGGAGACC GACGATCTGC TCGACGAAAT CGACGACGTC CTCGAGGAGA ACGCCGAGGA	60
CTTCGTCCGC GCATACGTCC AAAAGGGCGG ACA GTG ACC TGG CCG TTG CCC GAT	114
Met Thr Trp Pro Leu Pro Asp	
-55 -50	
CGC CTG TCC ATT AAT TCA CTC TCT GGA ACA CCC GCT GTA GAC CTA TCT	162
Arg Leu Ser Ile Asn Ser Leu Ser Gly Thr Pro Ala Val Asp Leu Ser	
-45 -40 -35	
TCT TTC ACT GAC TTC CTG CGC CGC CAG GCG CCG GAG TTG CTG CCG GCA	210
Ser Phe Thr Asp Phe Leu Arg Arg Gln Ala Pro Glu Leu Leu Pro Ala	
-30 -25 -20	
AGC ATC AGC GGC GGT GCG CCA CTC GCA GGC GGC GAT GCG CAA CTG CCG	258
Ser Ile Ser Gly Gly Ala Pro Leu Ala Gly Gly Asp Ala Gln Leu Pro	
-15 -10 -5	
CAC GGC ACC ACC ATT GTC GCG CTG AAA TAC CCC GGC GGT GTT GTC ATG	306
His Gly Thr Thr Ile Val Ala Leu Lys Tyr Pro Gly Gly Val Val Met	
1 5 10 15	
GCG GGT GAC CGG CGT TCG ACG CAG GGC AAC ATG ATT TCT GGG CGT GAT	354
Ala Gly Asp Arg Arg Ser Thr Gln Gly Asn Met Ile Ser Gly Arg Asp	
20 25 30	
GTG CGC AAG GTG TAT ATC ACC GAT GAC TAC ACC GCT ACC GGC ATC GCT	402
Val Arg Lys Val Tyr Ile Thr Asp Asp Tyr Thr Ala Thr Gly Ile Ala	
35 40 45	
GGC ACG GCT GCG GTC GCG GTT GAG TTT GCC CGG CTG TAT GCC GTG GAA	450
Gly Thr Ala Ala Val Ala Val Glu Phe Ala Arg Leu Tyr Ala Val Glu	
50 55 60	
CTT GAG CAC TAC GAG AAG CTC GAG GGT GTG CCG CTG ACG TTT GCC GGC	498
Leu Glu His Tyr Glu Lys Leu Glu Gly Val Pro Leu Thr Phe Ala Gly	
65 70 75	

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AAA ATC AAC CGG CTG GCG ATT ATG GTG CGT GGC AAT CTG GCG GCC GCG	546
Lys Ile Asn Arg Leu Ala Ile Met Val Arg Gly Asn Leu Ala Ala Ala	
80 85 90 95	
ATG CAG GGT CTG CTG GCG TTG CCG TTG CTG GCG GGC TAC GAC ATT CAT	594
Met Gln Gly Leu Leu Ala Leu Pro Leu Leu Ala Gly Tyr Asp Ile His	
100 105 110	
GCG TCT GAC CCG CAG AGC GCG GGT CGT ATC GTT TCG TTC GAC GCC GCC	642
Ala Ser Asp Pro Gln Ser Ala Gly Arg Ile Val Ser Phe Asp Ala Ala	
115 120 125	
GGC GGT TGG AAC ATC GAG GAA GAG GGC TAT CAG GCG GTG GGC TCG GGT	690
Gly Gly Trp Asn Ile Glu Glu Glu Gly Tyr Gln Ala Val Gly Ser Gly	
130 135 140	
TCG CTG TTC GCG AAG TCG TCG ATG AAG AAG TTG TAT TCG CAG GTT ACC	738
Ser Leu Phe Ala Lys Ser Ser Met Lys Lys Leu Tyr Ser Gln Val Thr	
145 150 155	
GAC GGT GAT TCG GGG CTG CGG GTG GCG GTC GAG GCG CTC TAC GAC GCC	786
Asp Gly Asp Ser Gly Leu Arg Val Ala Val Glu Ala Leu Tyr Asp Ala	
160 165 170 175	
GCC GAC GAC GAC TCC GCC ACC GGC GGT CCG GAC CTG GTG CGG GGC ATC	834
Ala Asp Asp Asp Ser Ala Thr Gly Gly Pro Asp Leu Val Arg Gly Ile	
180 185 190	
TTT CCG ACG GCG GTG ATC ATC GAC GCC GAC GGG GCG GTT GAC GTG CCG	882
Phe Pro Thr Ala Val Ile Ile Asp Ala Asp Gly Ala Val Asp Val Pro	
195 200 205	
GAG AGC CGG ATT GCC GAA TTG GCC CGC GCG ATC ATC GAA AGC CGT TCG	930
Glu Ser Arg Ile Ala Glu Leu Ala Arg Ala Ile Ile Glu Ser Arg Ser	
210 215 220	
GGT GCG GAT ACT TTC GGC TCC GAT GGC GGT GAG AAG TGAGTTTTCC GTATTT	982
Gly Ala Asp Thr Phe Gly Ser Asp Gly Gly Glu Lys	
225 230 235	
CATCTCGCCT GAGCAGGC	1000

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 1...56

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

Met Thr Trp Pro Leu Pro Asp Arg Leu Ser Ile Asn Ser Leu Ser Gly
 -55 -50 -45

Thr Pro Ala Val Asp Leu Ser Ser Phe Thr Asp Phe Leu Arg Arg Gln
 -40 -35 -30 -25

Ala Pro Glu Leu Leu Pro Ala Ser Ile Ser Gly Gly Ala Pro Leu Ala
 -20 -15 -10

Gly Gly Asp Ala Gln Leu Pro His Gly Thr Thr Ile Val Ala Leu Lys
 -5 1 5

Tyr Pro Gly Gly Val Val Met Ala Gly Asp Arg Arg Ser Thr Gln Gly
 10 15 20

Asn Met Ile Ser Gly Arg Asp Val Arg Lys Val Tyr Ile Thr Asp Asp
 25 30 35 40

Tyr Thr Ala Thr Gly Ile Ala Gly Thr Ala Ala Val Ala Val Glu Phe
 45 50 55

Ala Arg Leu Tyr Ala Val Glu Leu Glu His Tyr Glu Lys Leu Glu Gly
 60 65 70

Val Pro Leu Thr Phe Ala Gly Lys Ile Asn Arg Leu Ala Ile Met Val
 75 80 85

Arg Gly Asn Leu Ala Ala Ala Met Gln Gly Leu Leu Ala Leu Pro Leu
 90 95 100

Leu Ala Gly Tyr Asp Ile His Ala Ser Asp Pro Gln Ser Ala Gly Arg
 105 110 115 120

Ile Val Ser Phe Asp Ala Ala Gly Gly Trp Asn Ile Glu Glu Glu Gly
 125 130 135

Tyr Gln Ala Val Gly Ser Gly Ser Leu Phe Ala Lys Ser Ser Met Lys
 140 145 150

Lys Leu Tyr Ser Gln Val Thr Asp Gly Asp Ser Gly Leu Arg Val Ala
 155 160 165

Val Glu Ala Leu Tyr Asp Ala Ala Asp Asp Asp Ser Ala Thr Gly Gly
 170 175 180

Pro Asp Leu Val Arg Gly Ile Phe Pro Thr Ala Val Ile Ile Asp Ala
 185 190 195 200

Asp Gly Ala Val Asp Val Pro Glu Ser Arg Ile Ala Glu Leu Ala Arg
 205 210 215

Ala Ile Ile Glu Ser Arg Ser Gly Ala Asp Thr Phe Gly Ser Asp Gly
 220 225 230

Gly Glu Lys
235

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 66...808
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

TTGGCCCGCG CGATCATCGA AAGCCGTTTCG GGTGCGGATA CTTTCGGCTC CGATGGCGGT	60
GAGAA GTG AGT TTT CCG TAT TTC ATC TCG CCT GAG CAG GCG ATG CGC GAG	110
Met Ser Phe Pro Tyr Phe Ile Ser Pro Glu Gln Ala Met Arg Glu	
1 5 10 15	
CGC AGC GAG TTG GCG CGT AAG GGC ATT GCG CGG GCC AAA AGC GTG GTG	158
Arg Ser Glu Leu Ala Arg Lys Gly Ile Ala Arg Ala Lys Ser Val Val	
20 25 30	
GCG CTG GCC TAT GCC GGT GGT GTG CTG TTC GTC GCG GAG AAT CCG TCG	206
Ala Leu Ala Tyr Ala Gly Gly Val Leu Phe Val Ala Glu Asn Pro Ser	
35 40 45	
CGG TCG CTG CAG AAG ATC AGT GAG CTC TAC GAT CGG GTG GGT TTT GCG	254
Arg Ser Leu Gln Lys Ile Ser Glu Leu Tyr Asp Arg Val Gly Phe Ala	
50 55 60	
GCT GCG GGC AAG TTC AAC GAG TTC GAC AAT TTG CGC CGC GGC GGG ATC	302
Ala Ala Gly Lys Phe Asn Glu Phe Asp Asn Leu Arg Arg Gly Gly Ile	
65 70 75	
CAG TTC GCC GAC ACC CGC GGT TAC GCC TAT GAC CGT CGT GAC GTC ACG	350
Gln Phe Ala Asp Thr Arg Gly Tyr Ala Tyr Asp Arg Arg Asp Val Thr	
80 85 90 95	
GGT CGG CAG TTG GCC AAT GTC TAC GCG CAG ACT CTA GGC ACC ATC TTC	398
Gly Arg Gln Leu Ala Asn Val Tyr Ala Gln Thr Leu Gly Thr Ile Phe	
100 105 110	
ACC GAA CAG GCC AAG CCC TAC GAG GTT GAG TTG TGT GTG GCC GAG GTG	446
Thr Glu Gln Ala Lys Pro Tyr Glu Val Glu Leu Cys Val Ala Glu Val	
115 120 125	
GCG CAT TAC GGC GAG ACG AAA CGC CCT GAG TTG TAT CGT ATT ACC TAC	494
Ala His Tyr Gly Glu Thr Lys Arg Pro Glu Leu Tyr Arg Ile Thr Tyr	
130 135 140	

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GAC GGG TCG ATC GCC GAC GAG CCG CAT TTC GTG GTG ATG GGC GGC ACC	542
Asp Gly Ser Ile Ala Asp Glu Pro His Phe Val Met Gly Gly Thr	
145 150 155	
ACG GAG CCG ATC GCC AAC GCG CTC AAA GAG TCG TAT GCC GAG AAC GCC	590
Thr Glu Pro Ile Ala Asn Ala Leu Lys Glu Ser Tyr Ala Glu Asn Ala	
160 165 170 175	
AGC CTG ACC GAC GCC CTG CGT ATC GCG GTC GCT GCA TTG CGG GCC GGC	638
Ser Leu Thr Asp Ala Leu Arg Ile Ala Val Ala Ala Leu Arg Ala Gly	
180 185 190	
AGT GCC GAC ACC TCG GGT GGT GAT CAA CCC ACC CTT GGC GTG GCC AGC	686
Ser Ala Asp Thr Ser Gly Gly Asp Gln Pro Thr Leu Gly Val Ala Ser	
195 200 205	
TTA GAG GTG GCC GTT CTC GAT GCC AAC CGG CCA CGG CGC GCG TTC CGG	734
Leu Glu Val Ala Val Leu Asp Ala Asn Arg Pro Arg Arg Ala Phe Arg	
210 215 220	
CGC ATC ACC GGC TCC GCC CTG CAA GCG TTG CTG GTA GAC CAG GAA AGC	782
Arg Ile Thr Gly Ser Ala Leu Gln Ala Leu Leu Val Asp Gln Glu Ser	
225 230 235	
CCG CAG TCT GAC GGC GAA TCG TCG GG CTGAGTCCGA AAGTCCGACG CGTGTCTG	836
Pro Gln Ser Asp Gly Glu Ser Ser Gly	
240 245	
GGACCCCGCT GCGACGTAA CTGCGCCTAA CCCC GGCTCG ACGCGTCGCC GGCCGTCCTG	896
ACTT	900

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met Ser Phe Pro Tyr Phe Ile Ser Pro Glu Gln Ala Met Arg Glu Arg	
1 5 10 15	
Ser Glu Leu Ala Arg Lys Gly Ile Ala Arg Ala Lys Ser Val Val Ala	
20 25 30	
Leu Ala Tyr Ala Gly Gly Val Leu Phe Val Ala Glu Asn Pro Ser Arg	
35 40 45	
Ser Leu Gln Lys Ile Ser Glu Leu Tyr Asp Arg Val Gly Phe Ala Ala	
50 55 60	

170

Ala Gly Lys Phe Asn Glu Phe Asp Asn Leu Arg Arg Gly Gly Ile Gln
 65 70 75 80

Phe Ala Asp Thr Arg Gly Tyr Ala Tyr Asp Arg Arg Asp Val Thr Gly
 85 90 95

Arg Gln Leu Ala Asn Val Tyr Ala Gln Thr Leu Gly Thr Ile Phe Thr
 100 105 110

Glu Gln Ala Lys Pro Tyr Glu Val Glu Leu Cys Val Ala Glu Val Ala
 115 120 125

His Tyr Gly Glu Thr Lys Arg Pro Glu Leu Tyr Arg Ile Thr Tyr Asp
 130 135 140

Gly Ser Ile Ala Asp Glu Pro His Phe Val Val Met Gly Gly Thr Thr
 145 150 155 160

Glu Pro Ile Ala Asn Ala Leu Lys Glu Ser Tyr Ala Glu Asn Ala Ser
 165 170 175

Leu Thr Asp Ala Leu Arg Ile Ala Val Ala Ala Leu Arg Ala Gly Ser
 180 185 190

Ala Asp Thr Ser Gly Gly Asp Gln Pro Thr Leu Gly Val Ala Ser Leu
 195 200 205

Glu Val Ala Val Leu Asp Ala Asn Arg Pro Arg Arg Ala Phe Arg Arg
 210 215 220

Ile Thr Gly Ser Ala Leu Gln Ala Leu Leu Val Asp Gln Glu Ser Pro
 225 230 235 240

Gln Ser Asp Gly Glu Ser Ser Gly
 245

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 98...1487
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

GAGTCATTGC CTGGTCGGCG TCATTCCGTA CTAGTCGGTT GTCGGACTTG ACCTACTGGG 60
 TCAGGCCGAC GAGCACTCGA CCATTAGGTT AGGGGCC GTG ACC CAC TAT GAC GTC 115
 Met Thr His Tyr Asp Val
 1 5

171

GTC	GTT	CTC	GGA	GCC	GGT	CCC	GGC	GGG	TAT	GTC	GCG	GCG	ATT	CGC	GCC	163
Val	Val	Leu	Gly	Ala	Gly	Pro	Gly	Gly	Tyr	Val	Ala	Ala	Ile	Arg	Ala	
			10					15					20			
GCA	CAG	CTC	GGC	CTG	AGC	ACT	GCA	ATC	GTC	GAA	CCC	AAG	TAC	TGG	GGC	211
Ala	Gln	Leu	Gly	Leu	Ser	Thr	Ala	Ile	Val	Glu	Pro	Lys	Tyr	Trp	Gly	
		25					30					35				
GGA	GTA	TGC	CTC	AAT	GTC	GGC	TGT	ATC	CCA	TCC	AAG	GCG	CTG	TTG	CGC	259
Gly	Val	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	Arg	
	40					45					50					
AAC	GCC	GAA	CTG	GTC	CAC	ATC	TTC	ACC	AAG	GAC	GCC	AAA	GCA	TTT	GGC	307
Asn	Ala	Glu	Leu	Val	His	Ile	Phe	Thr	Lys	Asp	Ala	Lys	Ala	Phe	Gly	
55					60					65					70	
ATC	AGC	GGC	GAG	GTG	ACC	TTC	GAC	TAC	GGC	ATC	GCC	TAT	GAC	CGC	AGC	355
Ile	Ser	Gly	Glu	Val	Thr	Phe	Asp	Tyr	Gly	Ile	Ala	Tyr	Asp	Arg	Ser	
			75					80						85		
CGA	AAG	GTA	GCC	GAG	GGC	AGG	GTG	GCC	GGT	GTG	CAC	TTC	CTG	ATG	AAG	403
Arg	Lys	Val	Ala	Glu	Gly	Arg	Val	Ala	Gly	Val	His	Phe	Leu	Met	Lys	
		90					95						100			
AAG	AAC	AAG	ATC	ACC	GAG	ATC	CAC	GGG	TAC	GGC	ACA	TTT	GCC	GAC	GCC	451
Lys	Asn	Lys	Ile	Thr	Glu	Ile	His	Gly	Tyr	Gly	Thr	Phe	Ala	Asp	Ala	
		105					110					115				
AAC	ACG	TTG	TTG	GTT	GAT	CTC	AAC	GAC	GGC	GGT	ACA	GAA	TCG	GTC	ACG	499
Asn	Thr	Leu	Leu	Val	Asp	Leu	Asn	Asp	Gly	Gly	Thr	Glu	Ser	Val	Thr	
	120					125					130					
TTC	GAC	AAC	GCC	ATC	ATC	GCG	ACC	GGC	AGT	AGC	ACC	CGG	CTG	GTT	CCC	547
Phe	Asp	Asn	Ala	Ile	Ile	Ala	Thr	Gly	Ser	Ser	Thr	Arg	Leu	Val	Pro	
135					140					145					150	
GGC	ACC	TCA	CTG	TCG	GCC	AAC	GTA	GTC	ACC	TAC	GAG	GAA	CAG	ATC	CTG	595
Gly	Thr	Ser	Leu	Ser	Ala	Asn	Val	Val	Thr	Tyr	Glu	Glu	Gln	Ile	Leu	
			155						160					165		
TCC	CGA	GAG	CTG	CCG	AAA	TCG	ATC	ATT	ATT	GCC	GGA	GCT	GGT	GCC	ATT	643
Ser	Arg	Glu	Leu	Pro	Lys	Ser	Ile	Ile	Ile	Ala	Gly	Ala	Gly	Ala	Ile	
			170				175						180			
GGC	ATG	GAG	TTC	GGC	TAC	GTG	CTG	AAG	AAC	TAC	GGC	GTT	GAC	GTG	ACC	691
Gly	Met	Glu	Phe	Gly	Tyr	Val	Leu	Lys	Asn	Tyr	Gly	Val	Asp	Val	Thr	
		185					190					195				
ATC	GTG	GAA	TTC	CTT	CCG	CGG	GCG	CTG	CCC	AAC	GAG	GAC	GCC	GAT	GTG	739
Ile	Val	Glu	Phe	Leu	Pro	Arg	Ala	Leu	Pro	Asn	Glu	Asp	Ala	Asp	Val	
	200					205					210					
TCC	AAG	GAG	ATC	GAG	AAG	CAG	TTC	AAA	AAG	CTG	GGT	GTC	ACG	ATC	CTG	787
Ser	Lys	Glu	Ile	Glu	Lys	Gln	Phe	Lys	Lys	Leu	Gly	Val	Thr	Ile	Leu	
215					220					225					230	
ACC	GCC	ACG	AAG	GTC	GAG	TCC	ATC	GCC	GAT	GGC	GGG	TCG	CAG	GTC	ACC	835
Thr	Ala	Thr	Lys	Val	Glu	Ser	Ile	Ala	Asp	Gly	Gly	Ser	Gln	Val	Thr	

235							240							245							
GTG	ACC	GTC	ACC	AAG	GAC	GGC	GTG	GCG	CAA	GAG	CTT	AAG	GCG	GAA	AAG						883
Val	Thr	Val	Thr	Lys	Asp	Gly	Val	Ala	Gln	Glu	Leu	Lys	Ala	Glu	Lys						
				250				255					260								
GTG	TTG	CAG	GCC	ATC	GGA	TTT	GCG	CCC	AAC	GTC	GAA	GGG	TAC	GGG	CTG						931
Val	Leu	Gln	Ala	Ile	Gly	Phe	Ala	Pro	Asn	Val	Glu	Gly	Tyr	Gly	Leu						
		265					270					275									
GAC	AAG	GCA	GGC	GTC	GCG	CTG	ACC	GAC	CGC	AAG	GCT	ATC	GGT	GTC	GAC						979
Asp	Lys	Ala	Gly	Val	Ala	Leu	Thr	Asp	Arg	Lys	Ala	Ile	Gly	Val	Asp						
	280					285					290										
GAC	TAC	ATG	CGT	ACC	AAC	GTG	GGC	CAC	ATC	TAC	GCT	ATC	GGC	GAT	GTC						1027
Asp	Tyr	Met	Arg	Thr	Asn	Val	Gly	His	Ile	Tyr	Ala	Ile	Gly	Asp	Val						
	295				300					305					310						
AAT	GGA	TTA	CTG	CAG	CTG	GCG	CAC	GTC	GCC	GAG	GCA	CAA	GGC	GTG	GTA						1075
Asn	Gly	Leu	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Val	Val						
				315					320					325							
GCC	GCC	GAA	ACC	ATT	GCC	GGT	GCA	GAG	ACT	TTG	ACG	CTG	GGC	GAC	CAT						1123
Ala	Ala	Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Leu	Thr	Leu	Gly	Asp	His						
			330					335					340								
CGG	ATG	TTG	CCG	CGC	GCG	ACG	TTC	TGT	CAG	CCA	AAC	GTT	GCC	AGC	TTC						1171
Arg	Met	Leu	Pro	Arg	Ala	Thr	Phe	Cys	Gln	Pro	Asn	Val	Ala	Ser	Phe						
		345					350					355									
GGG	CTC	ACC	GAG	CAG	CAA	GCC	CGC	AAC	GAA	GGT	TAC	GAC	GTG	GTG	GTG						1219
Gly	Leu	Thr	Glu	Gln	Gln	Ala	Arg	Asn	Glu	Gly	Tyr	Asp	Val	Val	Val						
	360					365					370										
GCC	AAG	TTC	CCG	TTC	ACG	GCC	AAC	GCC	AAG	GCG	CAC	GGC	GTG	GGT	GAC						1267
Ala	Lys	Phe	Pro	Phe	Thr	Ala	Asn	Ala	Lys	Ala	His	Gly	Val	Gly	Asp						
	375				380				385						390						
CCC	AGT	GGG	TTC	GTC	AAG	CTG	GTG	GCC	GAC	GCC	AAG	CAC	GGC	GAG	CTA						1315
Pro	Ser	Gly	Phe	Val	Lys	Leu	Val	Ala	Asp	Ala	Lys	His	Gly	Glu	Leu						
				395					400					405							
CTG	GGT	GGG	CAC	CTG	GTC	GGC	CAC	GAC	GTG	GCC	GAG	CTG	CTG	CCG	GAG						1363
Leu	Gly	Gly	His	Leu	Val	Gly	His	Asp	Val	Ala	Glu	Leu	Leu	Pro	Glu						
			410					415					420								
CTC	ACG	CTG	GCG	CAG	AGG	TGG	GAC	CTG	ACC	GCC	AGC	GAG	CTG	GCT	CGC						1411
Leu	Thr	Leu	Ala	Gln	Arg	Trp	Asp	Leu	Thr	Ala	Ser	Glu	Leu	Ala	Arg						
		425					430					435									
AAC	GTC	CAC	ACC	CAC	CCA	ACG	ATG	TCT	GAG	GCG	CTG	CAG	GAG	TGC	TTC						1459
Asn	Val	His	Thr	His	Pro	Thr	Met	Ser	Glu	Ala	Leu	Gln	Glu	Cys	Phe						
	440					445					450										
CAC	GGC	CTG	GTT	GGC	CAC	ATG	ATC	AAT	T	TCTGAGCGGC	TCATGACGAG	GCGCG									1512
His	Gly	Leu	Val	Gly	His	Met	Ile	Asn	Phe												
	455				460																

CGAGCACTGA CACCCCCCAG ATCATCATGG GTGCCATCGG TGGTGTGG

1560

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

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Met Thr His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr
 1          5          10          15
Val Ala Ala Ile Arg Ala Ala Gln Leu Gly Leu Ser Thr Ala Ile Val
          20          25          30
Glu Pro Lys Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro
          35          40          45
Ser Lys Ala Leu Leu Arg Asn Ala Glu Leu Val His Ile Phe Thr Lys
          50          55          60
Asp Ala Lys Ala Phe Gly Ile Ser Gly Glu Val Thr Phe Asp Tyr Gly
65          70          75          80
Ile Ala Tyr Asp Arg Ser Arg Lys Val Ala Glu Gly Arg Val Ala Gly
          85          90          95
Val His Phe Leu Met Lys Lys Asn Lys Ile Thr Glu Ile His Gly Tyr
          100          105          110
Gly Thr Phe Ala Asp Ala Asn Thr Leu Leu Val Asp Leu Asn Asp Gly
          115          120          125
Gly Thr Glu Ser Val Thr Phe Asp Asn Ala Ile Ile Ala Thr Gly Ser
          130          135          140
Ser Thr Arg Leu Val Pro Gly Thr Ser Leu Ser Ala Asn Val Val Thr
145          150          155          160
Tyr Glu Glu Gln Ile Leu Ser Arg Glu Leu Pro Lys Ser Ile Ile Ile
          165          170          175
Ala Gly Ala Gly Ala Ile Gly Met Glu Phe Gly Tyr Val Leu Lys Asn
          180          185          190
Tyr Gly Val Asp Val Thr Ile Val Glu Phe Leu Pro Arg Ala Leu Pro
          195          200          205
Asn Glu Asp Ala Asp Val Ser Lys Glu Ile Glu Lys Gln Phe Lys Lys
          210          215          220
Leu Gly Val Thr Ile Leu Thr Ala Thr Lys Val Glu Ser Ile Ala Asp
225          230          235          240
Gly Gly Ser Gln Val Thr Val Thr Val Thr Lys Asp Gly Val Ala Gln
          245          250          255
Glu Leu Lys Ala Glu Lys Val Leu Gln Ala Ile Gly Phe Ala Pro Asn
          260          265          270
Val Glu Gly Tyr Gly Leu Asp Lys Ala Gly Val Ala Leu Thr Asp Arg
          275          280          285
Lys Ala Ile Gly Val Asp Asp Tyr Met Arg Thr Asn Val Gly His Ile
          290          295          300
Tyr Ala Ile Gly Asp Val Asn Gly Leu Leu Gln Leu Ala His Val Ala
305          310          315          320
Glu Ala Gln Gly Val Val Ala Ala Glu Thr Ile Ala Gly Ala Glu Thr
          325          330          335
Leu Thr Leu Gly Asp His Arg Met Leu Pro Arg Ala Thr Phe Cys Gln

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			340				345				350				
Pro	Asn	Val	Ala	Ser	Phe	Gly	Leu	Thr	Glu	Gln	Gln	Ala	Arg	Asn	Glu
			355				360				365				
Gly	Tyr	Asp	Val	Val	Val	Ala	Lys	Phe	Pro	Phe	Thr	Ala	Asn	Ala	Lys
			370				375				380				
Ala	His	Gly	Val	Gly	Asp	Pro	Ser	Gly	Phe	Val	Lys	Leu	Val	Ala	Asp
			385				390				395				
Ala	Lys	His	Gly	Glu	Leu	Leu	Gly	Gly	His	Leu	Val	Gly	His	Asp	Val
			405				410				415				
Ala	Glu	Leu	Leu	Pro	Glu	Leu	Thr	Leu	Ala	Gln	Arg	Trp	Asp	Leu	Thr
			420				425				430				
Ala	Ser	Glu	Leu	Ala	Arg	Asn	Val	His	Thr	His	Pro	Thr	Met	Ser	Glu
			435				440				445				
Ala	Leu	Gln	Glu	Cys	Phe	His	Gly	Leu	Val	Gly	His	Met	Ile	Asn	Phe
			450				455				460				

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 550 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 101...490
(D) OTHER INFORMATION:

GGCCCCGGCTC	GCGGCCGCC	TGCAGGAAAA	GAAGGCCTGC	CCAGGCCCAG	ACTCAGCCGA	60
GTAGTCACCC	AGTACCCAC	ACCAGGAAGG	ACCGCCCATC	ATG	GCA AAG CTC TCC	115
				Met	Ala Lys Leu Ser	
				1	5	
ACC GAC GAA CTG CTG GAC GCG TTC AAG GAA ATG ACC CTG TTG GAG CTC	163					
Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met Thr Leu Leu Glu Leu						
10 15 20						
TCC GAC TTC GTC AAG AAG TTC GAG GAG ACC TTC GAG GTC ACC GCC GCC	211					
Ser Asp Phe Val Lys Lys Phe Glu Glu Thr Phe Glu Val Thr Ala Ala						
25 30 35						
GCT CCA GTC GCC GTC GCC GCC GCC GGT GCC GCC CCG GCC GGT GCC GCC	259					
Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala Pro Ala Gly Ala Ala						
40 45 50						
GTC GAG GCT GCC GAG GAG CAG TCC GAG TTC GAC GTG ATC CTT GAG GCC	307					
Val Glu Ala Ala Glu Glu Gln Ser Glu Phe Asp Val Ile Leu Glu Ala						
55 60 65						
GCC GGC GAC AAG AAG ATC GGC GTC ATC AAG GTG GTC CGG GAG ATC GTT	355					
Ala Gly Asp Lys Lys Ile Gly Val Ile Lys Val Val Arg Glu Ile Val						
70 75 80 85						

175

TCC GGC CTG GGC CTC AAG GAG GCC AAG GAC CTG GTC GAC GGC GCG CCC 403
 Ser Gly Leu Gly Leu Lys Glu Ala Lys Asp Leu Val Asp Gly Ala Pro
 90 95 100

AAG CCG CTG CTG GAG AAG GTC GCC AAG GAG GCC GCC GAC GAG GCC AAG 451
 Lys Pro Leu Leu Glu Lys Val Ala Lys Glu Ala Ala Asp Glu Ala Lys
 105 110 115

GCC AAG CTG GAG GCC GCC GGC GCC ACC GTC ACC GTC AAG TAGCTCTGCC CA 502
 Ala Lys Leu Glu Ala Ala Gly Ala Thr Val Thr Val Lys
 120 125 130

GCGTGTTCCTT TTGCGTCTGC TCGGCCCGTA GCGAACACTG CGCCCGCT 550

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

Met Ala Lys Leu Ser Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met
 1 5 10 15

Thr Leu Leu Glu Leu Ser Asp Phe Val Lys Lys Phe Glu Glu Thr Phe
 20 25 30

Glu Val Thr Ala Ala Ala Pro Val Ala Val Ala Ala Ala Gly Ala Ala
 35 40 45

Pro Ala Gly Ala Ala Val Glu Ala Ala Glu Glu Gln Ser Glu Phe Asp
 50 55 60

Val Ile Leu Glu Ala Ala Gly Asp Lys Lys Ile Gly Val Ile Lys Val
 65 70 75 80

Val Arg Glu Ile Val Ser Gly Leu Gly Leu Lys Glu Ala Lys Asp Leu
 85 90 95

Val Asp Gly Ala Pro Lys Pro Leu Leu Glu Lys Val Ala Lys Glu Ala
 100 105 110

Ala Asp Glu Ala Lys Ala Lys Leu Glu Ala Ala Gly Ala Thr Val Thr
 115 120 125

Val Lys
 130

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

176

- (A) LENGTH: 900 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 87...770
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TGAACGCCAT CGGGTCCAAC GAACGCAGCG CTACCTGATC ACCACCGGGT CTGTTAGGGC	60
TCTTCCCCAG GTCGTACAGT CGGGCC ATG GCC ATT GAG GTT TCG GTG TTG CGG	113
Met Ala Ile Glu Val Ser Val Leu Arg	
1 5	
GTT TTC ACC GAT TCA GAC GGG AAT TTC GGT AAT CCG CTG GGG GTG ATC	161
Val Phe Thr Asp Ser Asp Gly Asn Phe Gly Asn Pro Leu Gly Val Ile	
10 15 20 25	
AAC GCC AGC AAG GTC GAA CAC CGC GAC AGG CAG CAG CTG GCA GCC CAA	209
Asn Ala Ser Lys Val Glu His Arg Asp Arg Gln Gln Leu Ala Ala Gln	
30 35 40	
TCG GGC TAC AGC GAA ACC ATA TTC GTC GAT CTT CCC AGC CCC GGC TCA	257
Ser Gly Tyr Ser Glu Thr Ile Phe Val Asp Leu Pro Ser Pro Gly Ser	
45 50 55	
ACC ACC GCA CAC GCC ACC ATC CAT ACT CCC CGC ACC GAA ATT CCG TTC	305
Thr Thr Ala His Ala Thr Ile His Thr Pro Arg Thr Glu Ile Pro Phe	
60 65 70	
GCC GGA CAC CCG ACC GTG GGA GCG TCC TGG TGG CTG CGC GAG AGG GGG	353
Ala Gly His Pro Thr Val Gly Ala Ser Trp Trp Leu Arg Glu Arg Gly	
75 80 85	
ACG CCA ATT AAC ACG CTG CAG GTG CCG GCC GGC ATC GTC CAG GTG AGC	401
Thr Pro Ile Asn Thr Leu Gln Val Pro Ala Gly Ile Val Gln Val Ser	
90 95 100 105	
TAC CAC GGT GAT CTC ACC GCC ATC AGC GCC CGC TCG GAA TGG GCA CCC	449
Tyr His Gly Asp Leu Thr Ala Ile Ser Ala Arg Ser Glu Trp Ala Pro	
110 115 120	
GAG TTC GCC ATC CAC GAC CTG GAT TCA CTT GAT GCG CTT GCC GCC GCC	497
Glu Phe Ala Ile His Asp Leu Asp Ser Leu Asp Ala Leu Ala Ala Ala	
125 130 135	
GAC CCC GCC GAC TTT CCG GAC GAC ATC GCG CAC TAC CTC TGG ACC TGG	545
Asp Pro Ala Asp Phe Pro Asp Asp Ile Ala His Tyr Leu Trp Thr Trp	
140 145 150	
ACC GAC CGC TCC GCT GGC TCG CTG CGC GCC CGC ATG TTT GCC GCC AAC	593
Thr Asp Arg Ser Ala Gly Ser Leu Arg Ala Arg Met Phe Ala Ala Asn	

177

155	160	165	
TTG GGC GTC ACC GAA GAC GAA GCG ACC GGT GCC GCG GCC ATC CGG ATT			641
Leu Gly Val Thr Glu Asp Glu Ala Thr Gly Ala Ala Ala Ile Arg Ile			
170	175	180	185
ACC GAT TAC CTC AGC CGT GAC CTC ACC ATC ACC CAG GGC AAA GGA TCG			689
Thr Asp Tyr Leu Ser Arg Asp Leu Thr Ile Thr Gln Gly Lys Gly Ser			
	190	195	200
TTG ATC CAC ACC ACC TGG AGT CCC GAG GGC TGG GTT CGG GTA GCC GGC			737
Leu Ile His Thr Thr Trp Ser Pro Glu Gly Trp Val Arg Val Ala Gly			
	205	210	215
CGA GTT GTC AGC GAC GGT GTG GCA CAA CTC GAC TGACGTAGAG CTCAGCGCTG			790
Arg Val Val Ser Asp Gly Val Ala Gln Leu Asp			
	220	225	
CCGATGCAAC ACGGCGGCAA GGTGATCCTG CAGGGGTTGC CCGACCGCGC GCATCTGCAA			850
CGAGTACGAA AGCTCGTCGC CGTCGATGCG GTAGGAACGG TCAAGGGCGG			900

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met	Ala	Ile	Glu	Val	Ser	Val	Leu	Arg	Val	Phe	Thr	Asp	Ser	Asp	Gly	
1				5					10					15		
Asn	Phe	Gly	Asn	Pro	Leu	Gly	Val	Ile	Asn	Ala	Ser	Lys	Val	Glu	His	
		20					25						30			
Arg	Asp	Arg	Gln	Gln	Leu	Ala	Ala	Gln	Ser	Gly	Tyr	Ser	Glu	Thr	Ile	
		35				40						45				
Phe	Val	Asp	Leu	Pro	Ser	Pro	Gly	Ser	Thr	Thr	Ala	His	Ala	Thr	Ile	
	50					55					60					
His	Thr	Pro	Arg	Thr	Glu	Ile	Pro	Phe	Ala	Gly	His	Pro	Thr	Val	Gly	
	65				70					75				80		
Ala	Ser	Trp	Trp	Leu	Arg	Glu	Arg	Gly	Thr	Pro	Ile	Asn	Thr	Leu	Gln	
				85				90						95		
Val	Pro	Ala	Gly	Ile	Val	Gln	Val	Ser	Tyr	His	Gly	Asp	Leu	Thr	Ala	
		100					105						110			
Ile	Ser	Ala	Arg	Ser	Glu	Trp	Ala	Pro	Glu	Phe	Ala	Ile	His	Asp	Leu	

178

115					120					125						
Asp	Ser	Leu	Asp	Ala	Leu	Ala	Ala	Ala	Asp	Pro	Ala	Asp	Phe	Pro	Asp	
130					135					140						
Asp	Ile	Ala	His	Tyr	Leu	Trp	Thr	Trp	Thr	Asp	Arg	Ser	Ala	Gly	Ser	
145					150					155					160	
Leu	Arg	Ala	Arg	Met	Phe	Ala	Ala	Asn	Leu	Gly	Val	Thr	Glu	Asp	Glu	
165					170					175						
Ala	Thr	Gly	Ala	Ala	Ala	Ile	Arg	Ile	Thr	Asp	Tyr	Leu	Ser	Arg	Asp	
180					185					190						
Leu	Thr	Ile	Thr	Gln	Gly	Lys	Gly	Ser	Leu	Ile	His	Thr	Thr	Trp	Ser	
195					200					205						
Pro	Glu	Gly	Trp	Val	Arg	Val	Ala	Gly	Arg	Val	Val	Ser	Asp	Gly	Val	
210					215					220						
Ala	Gln	Leu	Asp													
225																

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) **FEATURE:**

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 49...465
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GT	TTT	TG	TGG	TG	TCG	GT	TGG	TCT	GGG	GGG	CGCC	AACT	GGG	ATT	CGGT	TGGG	GTG	GGT	GCA	57
																		Met	Gly	Ala
																		1		
GGT	CCG	GCG	ATG	GGC	ATC	GGA	GGT	GTG	GGT	GGT	TTG	GGT	GGG	GCC	GGT					105
Gly	Pro	Ala	Met	Gly	Ile	Gly	Gly	Val	Gly	Gly	Leu	Gly	Gly	Gly	Ala	Gly				
	5						10				15									
TCG	GGT	CCG	GCG	ATG	GGC	ATG	GGG	GGT	GTG	GGT	GGT	TTG	GGT	GGG	GCC					153
Ser	Gly	Pro	Ala	Met	Gly	Met	Gly	Gly	Val	Gly	Gly	Leu	Gly	Gly	Ala					
	20					25				30					35					
GGT	TCG	GGT	CCG	GCG	ATG	GGC	ATG	GGG	GGT	GTG	GGT	GGT	TTA	GAT	GCG					201
Gly	Ser	Gly	Pro	Ala	Met	Gly	Met	Gly	Gly	Val	Gly	Gly	Gly	Leu	Asp	Ala				
				40					45					50						
GCC	GGT	TCC	GGC	GAG	GGC	GGC	TCT	CCT	GCG	GCG	ATC	GGC	ATC	GGA	GTT					249

179

Ala Gly Ser Gly Glu Gly Gly Ser Pro Ala Ala Ile Gly Ile Gly Val	
55 60 65	
GGC GGA GGC GGA GGT GGG GGT GGG GGT GGC GGC GGC GGG GCC GAC ACG	297
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Asp Thr	
70 75 80	
AAC CGC TCC GAC AGG TCG TCG GAC GTC GGG GGC GGA GTC TGG CCG TTG	345
Asn Arg Ser Asp Arg Ser Ser Asp Val Gly Gly Gly Val Trp Pro Leu	
85 90 95	
GGC TTC GGT AGG TTT GCC GAT GCG GGC GCC GGC GGA AAC GAA GCA CTG	393
Gly Phe Gly Arg Phe Ala Asp Ala Gly Ala Gly Gly Asn Glu Ala Leu	
100 105 110 115	
GGG TCG AAG AAC GGC TGC GCT GCC ATA TCG TCC GGA GCT TCC ATA CCT	441
Gly Ser Lys Asn Gly Cys Ala Ala Ile Ser Ser Gly Ala Ser Ile Pro	
120 125 130	
TCG TGC GGC CGG AAG AGC TTG TCG TAGTCGGCCG CCATGACAAC CTCTCAGAGT	495
Ser Cys Gly Arg Lys Ser Leu Ser	
135	
GCGCT	500

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Met Gly Ala Gly Pro Ala Met Gly Ile Gly Gly Val Gly Gly Leu Gly	
1 5 10 15	
Gly Ala Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly Leu	
20 25 30	
Gly Gly Ala Gly Ser Gly Pro Ala Met Gly Met Gly Gly Val Gly Gly	
35 40 45	
Leu Asp Ala Ala Gly Ser Gly Glu Gly Gly Ser Pro Ala Ala Ile Gly	
50 55 60	
Ile Gly Val Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly	
65 70 75 80	
Ala Asp Thr Asn Arg Ser Asp Arg Ser Ser Asp Val Gly Gly Gly Val	
85 90 95	
Trp Pro Leu Gly Phe Gly Arg Phe Ala Asp Ala Gly Ala Gly Gly Asn	

180

100	105	110
Glu Ala Leu Gly Ser Lys Asn Gly Cys Ala Ala Ile Ser Ser Gly Ala		
115	120	125
Ser Ile Pro Ser Cys Gly Arg Lys Ser Leu Ser		
130	135	

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2050 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 22...2019
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

AGCGCACTCT GAGAGGTTGT C ATG GCG GCC GAC TAC GAC AAG CTC TTC CGG	51
Met Ala Ala Asp Tyr Asp Lys Leu Phe Arg	
1 5 10	
CCG CAC GAA GGT ATG GAA GCT CCG GAC GAT ATG GCA GCG CAG CCG TTC	99
Pro His Glu Gly Met Glu Ala Pro Asp Asp Met Ala Ala Gln Pro Phe	
15 20 25	
TTC GAC CCC AGT GCT TCG TTT CCG CCG GCG CCC GCA TCG GCA AAC CTA	147
Phe Asp Pro Ser Ala Ser Phe Pro Pro Ala Pro Ala Ser Ala Asn Leu	
30 35 40	
CCG AAG CCC AAC GGC CAG ACT CCG CCC CCG ACG TCC GAC GAC CTG TCG	195
Pro Lys Pro Asn Gly Gln Thr Pro Pro Pro Thr Ser Asp Asp Leu Ser	
45 50 55	
GAG CGG TTC GTG TCG GCC CCG CCG CCG CCA CCC CCA CCC CCA CCT CCG	243
Glu Arg Phe Val Ser Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro	
60 65 70	
CCT CCG CCA ACT CCG ATG CCG ATC GCC GCA GGA GAG CCG CCC TCG CCG	291
Pro Pro Pro Thr Pro Met Pro Ile Ala Ala Gly Glu Pro Pro Ser Pro	
75 80 85 90	
GAA CCG GCC GCA TCT AAA CCA CCC ACA CCC CCC ATG CCC ATC GCC GGA	339
Glu Pro Ala Ala Ser Lys Pro Pro Thr Pro Pro Met Pro Ile Ala Gly	
95 100 105	
CCC GAA CCG GCC CCA CCC AAA CCA CCC ACA CCC CCC ATG CCC ATC GCC	387
Pro Glu Pro Ala Pro Pro Lys Pro Pro Thr Pro Pro Met Pro Ile Ala	
110 115 120	

181

GGA CCC GAA CCG GCC CCA CCC AAA CCA CCC ACA CCT CCG ATG CCC ATC	435
Gly Pro Glu Pro Ala Pro Pro Lys Pro Pro Thr Pro Pro Met Pro Ile	
125 130 135	
GCC GGA CCT GCA CCC ACC CCA ACC GAA TCC CAG TTG GCG CCC CCC AGA	483
Ala Gly Pro Ala Pro Thr Pro Thr Glu Ser Gln Leu Ala Pro Pro Arg	
140 145 150	
CCA CCG ACA CCA CAA ACG CCA ACC GGA GCG CCG CAG CAA CCG GAA TCA	531
Pro Pro Thr Pro Gln Thr Pro Thr Gly Ala Pro Gln Gln Pro Glu Ser	
155 160 165 170	
CCG GCG CCC CAC GTA CCC TCG CAC GGG CCA CAT CAA CCC CGG CGC ACC	579
Pro Ala Pro His Val Pro Ser His Gly Pro His Gln Pro Arg Arg Thr	
175 180 185	
GCA CCA GCA CCG CCC TGG GCA AAG ATG CCA ATC GGC GAA CCC CCG CCC	627
Ala Pro Ala Pro Pro Trp Ala Lys Met Pro Ile Gly Glu Pro Pro Pro	
190 195 200	
GCT CCG TCC AGA CCG TCT GCG TCC CCG GCC GAA CCA CCG ACC CGG CCG	675
Ala Pro Ser Arg Pro Ser Ala Ser Pro Ala Glu Pro Pro Thr Arg Pro	
205 210 215	
GCC CCC CAA CAC TCC CGA CGT GCG CGC CGG GGT CAC CGC TAT CGC ACA	723
Ala Pro Gln His Ser Arg Arg Ala Arg Arg Gly His Arg Tyr Arg Thr	
220 225 230	
GAC ACC GAA CGA AAC GTC GGG AAG GTA GCA ACT GGT CCA TCC ATC CAG	771
Asp Thr Glu Arg Asn Val Gly Lys Val Ala Thr Gly Pro Ser Ile Gln	
235 240 245 250	
GCG CGG CTG CGG GCA GAG GAA GCA TCC GGC GCG CAG CTC GCC CCC GGA	819
Ala Arg Leu Arg Ala Glu Glu Ala Ser Gly Ala Gln Leu Ala Pro Gly	
255 260 265	
ACG GAG CCC TCG CCA GCG CCG TTG GGC CAA CCG AGA TCG TAT CTG GCT	867
Thr Glu Pro Ser Pro Ala Pro Leu Gly Gln Pro Arg Ser Tyr Leu Ala	
270 275 280	
CCG CCC ACC CGC CCC GCG CCG ACA GAA CCT CCC CCC AGC CCC TCG CCG	915
Pro Pro Thr Arg Pro Ala Pro Thr Glu Pro Pro Pro Ser Pro Ser Pro	
285 290 295	
CAG CGC AAC TCC GGT CGG CGT GCC GAG CGA CGC GTC CAC CCC GAT TTA	963
Gln Arg Asn Ser Gly Arg Arg Ala Glu Arg Arg Val His Pro Asp Leu	
300 305 310	
GCC GCC CAA CAT GCC GCG GCG CAA CCT GAT TCA ATT ACG GCC GCA ACC	1011
Ala Ala Gln His Ala Ala Ala Gln Pro Asp Ser Ile Thr Ala Ala Thr	
315 320 325 330	
ACT GGC GGT CGT CGC CGC AAG CGT GCA GCG CCG GAT CTC GAC GCG ACA	1059
Thr Gly Gly Arg Arg Arg Lys Arg Ala Ala Pro Asp Leu Asp Ala Thr	
335 340 345	
CAG AAA TCC TTA AGG CCG GCG GCC AAG GGG CCG AAG GTG AAG AAG GTG	1107
Gln Lys Ser Leu Arg Pro Ala Ala Lys Gly Pro Lys Val Lys Lys Val	

350	355	360	
AAG CCC CAG AAA CCG AAG GCC ACG AAG CCG CCC AAA GTG GTG TCG CAG			1155
Lys Pro Gln Lys Pro Lys Ala Thr Lys Pro Pro Lys Val Val Ser Gln			
365	370	375	
CGC GGC TGG CGA CAT TGG GTG CAT GCG TTG ACG CGA ATC AAC CTG GGC			1203
Arg Gly Trp Arg His Trp Val His Ala Leu Thr Arg Ile Asn Leu Gly			
380	385	390	
CTG TCA CCC GAC GAG AAG TAC GAG CTG GAC CTG CAC GCT CGA GTC CGC			1251
Leu Ser Pro Asp Glu Lys Tyr Glu Leu Asp Leu His Ala Arg Val Arg			
395	400	405	410
CGC AAT CCC CGC GGG TCG TAT CAG ATC GCC GTC GTC GGT CTC AAA GGT			1299
Arg Asn Pro Arg Gly Ser Tyr Gln Ile Ala Val Val Gly Leu Lys Gly			
415	420	425	
GGG GCT GGC AAA ACC ACG CTG ACA GCA GCG TTG GGG TCG ACG TTG GCT			1347
Gly Ala Gly Lys Thr Thr Leu Thr Ala Ala Leu Gly Ser Thr Leu Ala			
430	435	440	
CAG GTG CGG GCC GAC CGG ATC CTG GCT CTA GAC GCG GAT CCA GGC GCC			1395
Gln Val Arg Ala Asp Arg Ile Leu Ala Leu Asp Ala Asp Pro Gly Ala			
445	450	455	
GGA AAC CTC GCC GAT CGG GTA GGG CGA CAA TCG GGC GCG ACC ATC GCT			1443
Gly Asn Leu Ala Asp Arg Val Gly Arg Gln Ser Gly Ala Thr Ile Ala			
460	465	470	
GAT GTG CTT GCA GAA AAA GAG CTG TCG CAC TAC AAC GAC ATC CGC GCA			1491
Asp Val Leu Ala Glu Lys Glu Leu Ser His Tyr Asn Asp Ile Arg Ala			
475	480	485	490
CAC ACT AGC GTC AAT GCG GTC AAT CTG GAA GTG CTG CCG GCA CCG GAA			1539
His Thr Ser Val Asn Ala Val Asn Leu Glu Val Leu Pro Ala Pro Glu			
495	500	505	
TAC AGC TCG GCG CAG CGC GCG CTC AGC GAC GCC GAC TGG CAT TTC ATC			1587
Tyr Ser Ser Ala Gln Arg Ala Leu Ser Asp Ala Asp Trp His Phe Ile			
510	515	520	
GCC GAT CCT GCG TCG AGG TTT TAC AAC CTC GTC TTG GCT GAT TGT GGG			1635
Ala Asp Pro Ala Ser Arg Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly			
525	530	535	
GCC GGC TTC TTC GAC CCG CTG ACC CGC GGC GTG CTG TCC ACG GTG TCC			1683
Ala Gly Phe Phe Asp Pro Leu Thr Arg Gly Val Leu Ser Thr Val Ser			
540	545	550	
GGT GTC GTG GTC GTG GCA AGT GTC TCA ATC GAC GGC GCA CAA CAG GCG			1731
Gly Val Val Val Val Ala Ser Val Ser Ile Asp Gly Ala Gln Gln Ala			
555	560	565	570
TCG GTC GCG TTG GAC TGG TTG CGC AAC AAC GGT TAC CAA GAT TTG GCG			1779
Ser Val Ala Leu Asp Trp Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala			
575	580	585	

183

AGC CGC GCA TGC GTG GTC ATC AAT CAC ATC ATG CCG GGA GAA CCC AAT	1827
Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro Gly Glu Pro Asn	
590 595 600	
GTC GCA GTT AAA GAC CTG GTG CGG CAT TTC GAA CAG CAA GTT CAA CCC	1875
Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln Gln Val Gln Pro	
605 610 615	
GGC CGG GTC GTG GTC ATG CCG TGG GAC AGG CAC ATT GCG GCC GGA ACC	1923
Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile Ala Ala Gly Thr	
620 625 630	
GAG ATT TCA CTC GAC TTG CTC GAC CCT ATC TAC AAG CGC AAG GTC CTC	1971
Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu	
635 640 645 650	
GAA TTG GCC GCA GCG CTA TCC GAC GAT TTC GAG AGG GCT GGA CGT CGT T	2020
Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg	
655 660 665	
GAGCGCACCT GCTGTTGCTG CTGGTCCTAC	2050

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Met	Ala	Ala	Asp	Tyr	Asp	Lys	Leu	Phe	Arg	Pro	His	Glu	Gly	Met	Glu
1				5					10					15	
Ala	Pro	Asp	Asp	Met	Ala	Ala	Gln	Pro	Phe	Phe	Asp	Pro	Ser	Ala	Ser
		20						25					30		
Phe	Pro	Pro	Ala	Pro	Ala	Ser	Ala	Asn	Leu	Pro	Lys	Pro	Asn	Gly	Gln
		35					40					45			
Thr	Pro	Pro	Pro	Thr	Ser	Asp	Asp	Leu	Ser	Glu	Arg	Phe	Val	Ser	Ala
	50					55					60				
Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Thr	Pro	Met
	65				70					75				80	
Pro	Ile	Ala	Ala	Gly	Glu	Pro	Pro	Ser	Pro	Glu	Pro	Ala	Ala	Ser	Lys
			85						90					95	
Pro	Pro	Thr	Pro	Pro	Met	Pro	Ile	Ala	Gly	Pro	Glu	Pro	Ala	Pro	Pro
		100						105					110		
Lys	Pro	Pro	Thr	Pro	Pro	Met	Pro	Ile	Ala	Gly	Pro	Glu	Pro	Ala	Pro

115	120	125
Pro Lys Pro Pro Thr Pro Pro Met Pro Ile Ala Gly Pro Ala Pro Thr		
130	135	140
Pro Thr Glu Ser Gln Leu Ala Pro Pro Arg Pro Pro Thr Pro Gln Thr		
145	150	155
Pro Thr Gly Ala Pro Gln Gln Pro Glu Ser Pro Ala Pro His Val Pro		
	165	170
Ser His Gly Pro His Gln Pro Arg Arg Thr Ala Pro Ala Pro Pro Trp		
	180	185
Ala Lys Met Pro Ile Gly Glu Pro Pro Pro Ala Pro Ser Arg Pro Ser		
	195	200
Ala Ser Pro Ala Glu Pro Pro Thr Arg Pro Ala Pro Gln His Ser Arg		
	210	215
Arg Ala Arg Arg Gly His Arg Tyr Arg Thr Asp Thr Glu Arg Asn Val		
225	230	235
Gly Lys Val Ala Thr Gly Pro Ser Ile Gln Ala Arg Leu Arg Ala Glu		
	245	250
Glu Ala Ser Gly Ala Gln Leu Ala Pro Gly Thr Glu Pro Ser Pro Ala		
	260	265
Pro Leu Gly Gln Pro Arg Ser Tyr Leu Ala Pro Pro Thr Arg Pro Ala		
	275	280
Pro Thr Glu Pro Pro Pro Ser Pro Ser Pro Gln Arg Asn Ser Gly Arg		
	290	295
Arg Ala Glu Arg Arg Val His Pro Asp Leu Ala Ala Gln His Ala Ala		
305	310	315
Ala Gln Pro Asp Ser Ile Thr Ala Ala Thr Thr Gly Gly Arg Arg Arg		
	325	330
Lys Arg Ala Ala Pro Asp Leu Asp Ala Thr Gln Lys Ser Leu Arg Pro		
	340	345
Ala Ala Lys Gly Pro Lys Val Lys Lys Val Lys Pro Gln Lys Pro Lys		
	355	360
Ala Thr Lys Pro Pro Lys Val Val Ser Gln Arg Gly Trp Arg His Trp		
	370	375
Val His Ala Leu Thr Arg Ile Asn Leu Gly Leu Ser Pro Asp Glu Lys		
385	390	395
Tyr Glu Leu Asp Leu His Ala Arg Val Arg Arg Asn Pro Arg Gly Ser		
	405	410
Tyr Gln Ile Ala Val Val Gly Leu Lys Gly Gly Ala Gly Lys Thr Thr		
	420	425
		430

185

Leu Thr Ala Ala Leu Gly Ser Thr Leu Ala Gln Val Arg Ala Asp Arg
 435 440 445
 Ile Leu Ala Leu Asp Ala Asp Pro Gly Ala Gly Asn Leu Ala Asp Arg
 450 455 460
 Val Gly Arg Gln Ser Gly Ala Thr Ile Ala Asp Val Leu Ala Glu Lys
 465 470 475 480
 Glu Leu Ser His Tyr Asn Asp Ile Arg Ala His Thr Ser Val Asn Ala
 485 490 495
 Val Asn Leu Glu Val Leu Pro Ala Pro Glu Tyr Ser Ser Ala Gln Arg
 500 505 510
 Ala Leu Ser Asp Ala Asp Trp His Phe Ile Ala Asp Pro Ala Ser Arg
 515 520 525
 Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly Ala Gly Phe Phe Asp Pro
 530 535 540
 Leu Thr Arg Gly Val Leu Ser Thr Val Ser Gly Val Val Val Val Ala
 545 550 555 560
 Ser Val Ser Ile Asp Gly Ala Gln Gln Ala Ser Val Ala Leu Asp Trp
 565 570 575
 Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala Ser Arg Ala Cys Val Val
 580 585 590
 Ile Asn His Ile Met Pro Gly Glu Pro Asn Val Ala Val Lys Asp Leu
 595 600 605
 Val Arg His Phe Glu Gln Gln Val Gln Pro Gly Arg Val Val Val Met
 610 615 620
 Pro Trp Asp Arg His Ile Ala Ala Gly Thr Glu Ile Ser Leu Asp Leu
 625 630 635 640
 Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu Glu Leu Ala Ala Ala Leu
 645 650 655
 Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg
 660 665

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 79...1851

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

GCAGCGATGA GGAGGAGCGG CGCCAACGGC CCGCGCCGGC GACGATGCAA AGCGCAGCGA	60
TGAGGAGGAG CGGCGCGC ATG ACT GCT GAA CCG GAA GTA CGG ACG CTG CGC Met Thr Ala Glu Pro Glu Val Arg Thr Leu Arg 1 5 10	111
GAG GTT GTG CTG GAC CAG CTC GGC ACT GCT GAA TCG CGT GCG TAC AAG Glu Val Val Leu Asp Gln Leu Gly Thr Ala Glu Ser Arg Ala Tyr Lys 15 20 25	159
ATG TGG CTG CCG CCG TTG ACC AAT CCG GTC CCG CTC AAC GAG CTC ATC Met Trp Leu Pro Pro Leu Thr Asn Pro Val Pro Leu Asn Glu Leu Ile 30 35 40	207
GCC CGT GAT CGG CGA CAA CCC CTG CGA TTT GCC CTG GGG ATC ATG GAT Ala Arg Asp Arg Arg Gln Pro Leu Arg Phe Ala Leu Gly Ile Met Asp 45 50 55	255
GAA CCG CGC CGC CAT CTA CAG GAT GTG TGG GGC GTA GAC GTT TCC GGG Glu Pro Arg Arg His Leu Gln Asp Val Trp Gly Val Asp Val Ser Gly 60 65 70 75	303
GCC GGC GGC AAC ATC GGT ATT GGG GGC GCA CCT CAA ACC GGG AAG TCG Ala Gly Gly Asn Ile Gly Ile Gly Gly Ala Pro Gln Thr Gly Lys Ser 80 85 90	351
ACG CTA CTG CAG ACG ATG GTG ATG TCG GCC GCC GCC ACA CAC TCA CCG Thr Leu Leu Gln Thr Met Val Met Ser Ala Ala Ala Thr His Ser Pro 95 100 105	399
CGC AAC GTT CAG TTC TAT TGC ATC GAC CTA GGT GGC GGC GGG CTG ATC Arg Asn Val Gln Phe Tyr Cys Ile Asp Leu Gly Gly Gly Gly Leu Ile 110 115 120	447
TAT CTC GAA AAC CTT CCA CAC GTC GGT GGG GTA GCC AAT CGG TCC GAG Tyr Leu Glu Asn Leu Pro His Val Gly Gly Val Ala Asn Arg Ser Glu 125 130 135	495
CCC GAC AAG GTC AAC CGG GTG GTC GCA GAG ATG CAA GCC GTC ATG CGG Pro Asp Lys Val Asn Arg Val Val Ala Glu Met Gln Ala Val Met Arg 140 145 150 155	543
CAA CGG GAA ACC ACC TTC AAG GAA CAC CGA GTG GGC TCG ATC GGG ATG Gln Arg Glu Thr Thr Phe Lys Glu His Arg Val Gly Ser Ile Gly Met 160 165 170	591
TAC CGG CAG CTG CGT GAC GAT CCA AGT CAA CCC GTT GCG TCC GAT CCA Tyr Arg Gln Leu Arg Asp Asp Pro Ser Gln Pro Val Ala Ser Asp Pro 175 180 185	639
TAC GGC GAC GTC TTT CTG ATC ATC GAC GGA TGG CCC GGT TTT GTC GGC Tyr Gly Asp Val Phe Leu Ile Ile Asp Gly Trp Pro Gly Phe Val Gly 190 195 200	687

187

GAG TTC CCC GAC CTT GAG GGG CAG GTT CAA GAT CTG GCC GCC CAG GGG Glu Phe Pro Asp Leu Glu Gly Gln Val Gln Asp Leu Ala Ala Gln Gly 205 210 215	735
CTG GGG TTC GGC GTC CAC GTC ATC ATC TCC ACG CCA CGC TGG ACA GAG Leu Gly Phe Gly Val His Val Ile Ile Ser Thr Pro Arg Trp Thr Glu 220 225 230 235	783
CTG AAG TCG CGT GTT CGC GAC TAC CTC GGC ACC AAG ATC GAG TTC CGG Leu Lys Ser Arg Val Arg Asp Tyr Leu Gly Thr Lys Ile Glu Phe Arg 240 245 250	831
CTT GGT GAC GTC AAT GAA ACC CAG ATC GAC CGG ATT ACC CGC GAG ATC Leu Gly Asp Val Asn Glu Thr Gln Ile Asp Arg Ile Thr Arg Glu Ile 255 260 265	879
CCG GCG AAT CGT CCG GGT CGG GCA GTG TCG ATG GAA AAG CAC CAT CTG Pro Ala Asn Arg Pro Gly Arg Ala Val Ser Met Glu Lys His His Leu 270 275 280	927
ATG ATC GGC GTG CCC AGG TTC GAC GGC GTG CAC AGC GCC GAT AAC CTG Met Ile Gly Val Pro Arg Phe Asp Gly Val His Ser Ala Asp Asn Leu 285 290 295	975
GTG GAG GCG ATC ACC GCG GGG GTG ACG CAG ATC GCT TCC CAG CAC ACC Val Glu Ala Ile Thr Ala Gly Val Thr Gln Ile Ala Ser Gln His Thr 300 305 310 315	1023
GAA CAG GCA CCT CCG GTG CGG GTC CTG CCG GAG CGT ATC CAC CTG CAC Glu Gln Ala Pro Pro Val Arg Val Leu Pro Glu Arg Ile His Leu His 320 325 330	1071
GAA CTC GAC CCG AAC CCG CCG GGA CCA GAG TCC GAC TAC CGC ACT CGC Glu Leu Asp Pro Asn Pro Pro Gly Pro Glu Ser Asp Tyr Arg Thr Arg 335 340 345	1119
TGG GAG ATT CCG ATC GGC TTG CGC GAG ACG GAC CTG ACG CCG GCT CAC Trp Glu Ile Pro Ile Gly Leu Arg Glu Thr Asp Leu Thr Pro Ala His 350 355 360	1167
TGC CAC ATG CAC ACG AAC CCG CAC CTA CTG ATC TTC GGT GCG GCC AAA Cys His Met His Thr Asn Pro His Leu Leu Ile Phe Gly Ala Ala Lys 365 370 375	1215
TCG GGC AAG ACG ACC ATT GCC CAC GCG ATC GCG CGC GCC ATT TGT GCC Ser Gly Lys Thr Thr Ile Ala His Ala Ile Ala Arg Ala Ile Cys Ala 380 385 390 395	1263
CGA AAC AGT CCC CAG CAG GTG CGG TTC ATG CTC GCG GAC TAC CGC TCG Arg Asn Ser Pro Gln Gln Val Arg Phe Met Leu Ala Asp Tyr Arg Ser 400 405 410	1311
GGC CTG CTG GAC GCG GTG CCG GAC ACC CAT CTG CTG GGC GCC GGC GCG Gly Leu Leu Asp Ala Val Pro Asp Thr His Leu Leu Gly Ala Gly Ala 415 420 425	1359
ATC AAC CGC AAC AGC GCG TCG CTA GAC GAG GCC GCT CAA GCA CTG GCG Ile Asn Arg Asn Ser Ala Ser Leu Asp Glu Ala Ala Gln Ala Leu Ala	1407

430	435	440	
GTC AAC CTG AAG AAG CGG TTG CCG CCG ACC GAC CTG ACG ACG GCG CAG			1455
Val Asn Leu Lys Lys Arg Leu Pro Pro Thr Asp Leu Thr Thr Ala Gln			
445	450	455	
CTA CGC TCG CGT TCG TGG TGG AGC GGA TTT GAC GTC GTG CTT CTG GTC			1503
Leu Arg Ser Arg Ser Trp Trp Ser Gly Phe Asp Val Val Leu Leu Val			
460	465	470	475
GAC GAT TGG CAC ATG ATC GTG GGT GCC GCC GGG GGG ATG CCG CCG ATG			1551
Asp Asp Trp His Met Ile Val Gly Ala Ala Gly Gly Met Pro Pro Met			
480	485	490	
GCA CCG CTG GCC CCG TTA TTG CCG GCG GCG GCA GAT ATC GGG TTG CAC			1599
Ala Pro Leu Ala Pro Leu Leu Pro Ala Ala Ala Asp Ile Gly Leu His			
495	500	505	
ATC ATT GTC ACC TGT CAG ATG AGC CAG GCT TAC AAG GCA ACC ATG GAC			1647
Ile Ile Val Thr Cys Gln Met Ser Gln Ala Tyr Lys Ala Thr Met Asp			
510	515	520	
AAG TTC GTC GGC GCC GCA TTC GGG TCG GGC GCT CCG ACA ATG TTC CTT			1695
Lys Phe Val Gly Ala Ala Phe Gly Ser Gly Ala Pro Thr Met Phe Leu			
525	530	535	
TCG GGC GAG AAG CAG GAA TTC CCA TCC AGT GAG TTC AAG GTC AAG CGG			1743
Ser Gly Glu Lys Gln Glu Phe Pro Ser Ser Glu Phe Lys Val Lys Arg			
540	545	550	555
CGC CCC CCT GGC CAG GCA TTT CTC GTC TCG CCA GAC GGC AAA GAG GTC			1791
Arg Pro Pro Gly Gln Ala Phe Leu Val Ser Pro Asp Gly Lys Glu Val			
560	565	570	
ATC CAG GCC CCC TAC ATC GAG CCT CCA GAA GAA GTG TTC GCA GCA CCC			1839
Ile Gln Ala Pro Tyr Ile Glu Pro Pro Glu Glu Val Phe Ala Ala Pro			
575	580	585	
CCA AGC GCC GGT TAAGATTATT TCATTGCCGG TGTAGCAGGA CCCGAGCTC			1890
Pro Ser Ala Gly			
590			

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Met	Thr	Ala	Glu	Pro	Glu	Val	Arg	Thr	Leu	Arg	Glu	Val	Val	Leu	Asp
1				5					10					15	

189

Gln Leu Gly Thr Ala Glu Ser Arg Ala Tyr Lys Met Trp Leu Pro Pro
 20 25 30

Leu Thr Asn Pro Val Pro Leu Asn Glu Leu Ile Ala Arg Asp Arg Arg
 35 40 45

Gln Pro Leu Arg Phe Ala Leu Gly Ile Met Asp Glu Pro Arg Arg His
 50 55 60

Leu Gln Asp Val Trp Gly Val Asp Val Ser Gly Ala Gly Gly Asn Ile
 65 70 75 80

Gly Ile Gly Gly Ala Pro Gln Thr Gly Lys Ser Thr Leu Leu Gln Thr
 85 90 95

Met Val Met Ser Ala Ala Ala Thr His Ser Pro Arg Asn Val Gln Phe
 100 105 110

Tyr Cys Ile Asp Leu Gly Gly Gly Gly Leu Ile Tyr Leu Glu Asn Leu
 115 120 125

Pro His Val Gly Gly Val Ala Asn Arg Ser Glu Pro Asp Lys Val Asn
 130 135 140

Arg Val Val Ala Glu Met Gln Ala Val Met Arg Gln Arg Glu Thr Thr
 145 150 155 160

Phe Lys Glu His Arg Val Gly Ser Ile Gly Met Tyr Arg Gln Leu Arg
 165 170 175

Asp Asp Pro Ser Gln Pro Val Ala Ser Asp Pro Tyr Gly Asp Val Phe
 180 185 190

Leu Ile Ile Asp Gly Trp Pro Gly Phe Val Gly Glu Phe Pro Asp Leu
 195 200 205

Glu Gly Gln Val Gln Asp Leu Ala Ala Gln Gly Leu Gly Phe Gly Val
 210 215 220

His Val Ile Ile Ser Thr Pro Arg Trp Thr Glu Leu Lys Ser Arg Val
 225 230 235 240

Arg Asp Tyr Leu Gly Thr Lys Ile Glu Phe Arg Leu Gly Asp Val Asn
 245 250 255

Glu Thr Gln Ile Asp Arg Ile Thr Arg Glu Ile Pro Ala Asn Arg Pro
 260 265 270

Gly Arg Ala Val Ser Met Glu Lys His His Leu Met Ile Gly Val Pro
 275 280 285

Arg Phe Asp Gly Val His Ser Ala Asp Asn Leu Val Glu Ala Ile Thr
 290 295 300

Ala Gly Val Thr Gln Ile Ala Ser Gln His Thr Glu Gln Ala Pro Pro
 305 310 315 320

Val Arg Val Leu Pro Glu Arg Ile His Leu His Glu Leu Asp Pro Asn

190

325										330					335				
Pro	Pro	Gly	Pro	Glu	Ser	Asp	Tyr	Arg	Thr	Arg	Trp	Glu	Ile	Pro	Ile				
			340					345					350						
Gly	Leu	Arg	Glu	Thr	Asp	Leu	Thr	Pro	Ala	His	Cys	His	Met	His	Thr				
		355					360					365							
Asn	Pro	His	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Lys	Ser	Gly	Lys	Thr	Thr				
		370				375						380							
Ile	Ala	His	Ala	Ile	Ala	Arg	Ala	Ile	Cys	Ala	Arg	Asn	Ser	Pro	Gln				
385					390					395					400				
Gln	Val	Arg	Phe	Met	Leu	Ala	Asp	Tyr	Arg	Ser	Gly	Leu	Leu	Asp	Ala				
				405					410					415					
Val	Pro	Asp	Thr	His	Leu	Leu	Gly	Ala	Gly	Ala	Ile	Asn	Arg	Asn	Ser				
			420					425					430						
Ala	Ser	Leu	Asp	Glu	Ala	Ala	Gln	Ala	Leu	Ala	Val	Asn	Leu	Lys	Lys				
		435					440					445							
Arg	Leu	Pro	Pro	Thr	Asp	Leu	Thr	Thr	Ala	Gln	Leu	Arg	Ser	Arg	Ser				
		450				455						460							
Trp	Trp	Ser	Gly	Phe	Asp	Val	Val	Leu	Leu	Val	Asp	Asp	Trp	His	Met				
465					470					475					480				
Ile	Val	Gly	Ala	Ala	Gly	Gly	Met	Pro	Pro	Met	Ala	Pro	Leu	Ala	Pro				
				485					490					495					
Leu	Leu	Pro	Ala	Ala	Ala	Asp	Ile	Gly	Leu	His	Ile	Ile	Val	Thr	Cys				
			500					505					510						
Gln	Met	Ser	Gln	Ala	Tyr	Lys	Ala	Thr	Met	Asp	Lys	Phe	Val	Gly	Ala				
		515					520					525							
Ala	Phe	Gly	Ser	Gly	Ala	Pro	Thr	Met	Phe	Leu	Ser	Gly	Glu	Lys	Gln				
		530				535					540								
Glu	Phe	Pro	Ser	Ser	Glu	Phe	Lys	Val	Lys	Arg	Arg	Pro	Pro	Gly	Gln				
545					550					555					560				
Ala	Phe	Leu	Val	Ser	Pro	Asp	Gly	Lys	Glu	Val	Ile	Gln	Ala	Pro	Tyr				
				565					570					575					
Ile	Glu	Pro	Pro	Glu	Glu	Val	Phe	Ala	Ala	Pro	Pro	Ser	Ala	Gly					
			580					585					590						

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

Asp	Pro	Val	Asp	Asp	Ala	Phe	Ile	Ala	Lys	Leu	Asn	Thr	Ala	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 14
- (C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

Asp	Pro	Val	Asp	Ala	Ile	Ile	Asn	Leu	Asp	Asn	Tyr	Gly	Xaa
1				5				10					

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) Feature:

- (A) NAME/KEY: Other
- (B) LOCATION: 5
- (C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

Ala	Glu	Met	Lys	Xaa	Phe	Lys	Asn	Ala	Ile	Val	Gln	Glu	Ile	Asp
1				5				10						15

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 3...3

(D) OTHER INFORMATION: Ala is Ala or Gln

(A) NAME/KEY: Other

(B) LOCATION: 7...7

(D) OTHER INFORMATION: Thr is Gly or Thr

(ix) Feature:

(A) NAME/KEY: Other

(B) LOCATION: 11

(C) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Val	Ile	Ala	Gly	Met	Val	Thr	His	Ile	His	Xaa	Val	Ala	Gly
1				5						10			

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

Thr	Asn	Ile	Val	Val	Leu	Ile	Lys	Gln	Val	Pro	Asp	Thr	Trp	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

Ala	Ile	Glu	Val	Ser	Val	Leu	Arg	Val	Phe	Thr	Asp	Ser	Asp	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 79:

193

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Ala Lys Leu Ser Thr Asp Glu Leu Leu Asp Ala Phe Lys Glu Met
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal
 (ix) FEATURE:

- (A) NAME/KEY: Other
 (B) LOCATION: 4...4
 (D) OTHER INFORMATION: Asp is Asp or Glu

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Asp Pro Ala Asp Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE: N-terminal

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val
 1 5 10 15

Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu
 20 25 30

Glu Ser Met Tyr Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr
 35 40 45

Val Ser

50

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

Thr	Thr	Ser	Pro	Asp	Pro	Tyr	Ala	Ala	Leu	Pro	Lys	Leu	Pro	Ser
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Thr	Glu	Tyr	Glu	Gly	Pro	Lys	Thr	Lys	Phe	His	Ala	Leu	Met	Gln
1				5				10						15

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Thr	Thr	Ile	Val	Ala	Leu	Lys	Tyr	Pro	Gly	Gly	Val	Val	Met	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 10
- (D) OTHER INFORMATION: Xaa is unknown

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 15
- (D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

Ser Phe Pro Tyr Phe Ile Ser Pro Glu Xaa Ala Met Arg Glu Xaa
 1             5             10             15

```

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

Thr His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr
 1             5             10             15

```

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 107...400
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

```

AGCCCGGTAA TCGAGTTCGG GCAATGCTGA CCATCGGGTT TGTTCCTGGC TATAACCGAA      60

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CGGTTTGTGT ACGGGATACA AATACAGGGA GGAAGAAGT AGGCAA ATG GAA AAA      115
                Met Glu Lys
                1

```

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ATG TCA CAT GAT CCG ATC GCT GCC GAC ATT GGC ACG CAA GTG AGC GAC 163
 Met Ser His Asp Pro Ile Ala Ala Asp Ile Gly Thr Gln Val Ser Asp
 5 10 15

 AAC GCT CTG CAC GGC GTG ACG GCC GGC TCG ACG GCG CTG ACG TCG GTG 211
 Asn Ala Leu His Gly Val Thr Ala Gly Ser Thr Ala Leu Thr Ser Val
 20 25 30 35

 ACC GGG CTG GTT CCC GCG GGG GCC GAT GAG GTC TCC GCC CAA GCG GCG 259
 Thr Gly Leu Val Pro Ala Gly Ala Asp Glu Val Ser Ala Gln Ala Ala
 40 45 50

 ACG GCG TTC ACA TCG GAG GGC ATC CAA TTG CTG GCT TCC AAT GCA TCG 307
 Thr Ala Phe Thr Ser Glu Gly Ile Gln Leu Leu Ala Ser Asn Ala Ser
 55 60 65

 GCC CAA GAC CAG CTC CAC CGT GCG GGC GAA GCG GTC CAG GAC GTC GCC 355
 Ala Gln Asp Gln Leu His Arg Ala Gly Glu Ala Val Gln Asp Val Ala
 70 75 80

 CGC ACC TAT TCG CAA ATC GAC GAC GGC GCC GCC GGC GTC TTC GCC TAATA 405
 Arg Thr Tyr Ser Gln Ile Asp Asp Gly Ala Ala Gly Val Phe Ala
 85 90 95

 GGCCCCAAC ACATCGGAGG GAGTGATCAC CATGCTGTGG CACGC 450

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Met Glu Lys Met Ser His Asp Pro Ile Ala Ala Asp Ile Gly Thr Gln
 1 5 10 15

 Val Ser Asp Asn Ala Leu His Gly Val Thr Ala Gly Ser Thr Ala Leu
 20 25 30

 Thr Ser Val Thr Gly Leu Val Pro Ala Gly Ala Asp Glu Val Ser Ala
 35 40 45

 Gln Ala Ala Thr Ala Phe Thr Ser Glu Gly Ile Gln Leu Leu Ala Ser
 50 55 60

 Asn Ala Ser Ala Gln Asp Gln Leu His Arg Ala Gly Glu Ala Val Gln
 65 70 75 80

 Asp Val Ala Arg Thr Tyr Ser Gln Ile Asp Asp Gly Ala Ala Gly Val
 85 90 95

 Phe Ala

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 37...453
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

GCAACCGGCT TTTCGATCAG CTGAGACATC AGCGGC GTG CGG GTC AAC GAC CCA	54
Met Arg Val Asn Asp Pro	
1 5	
CCT GCG CCA GGT AGC GAC TCC GCG CGC AGC AGG CCC GCG CCC GCG CTG	102
Pro Ala Pro Gly Ser Asp Ser Ala Arg Ser Arg Pro Ala Pro Ala Leu	
10 15 20	
GGG CCT GAT CCA CCA GCC AGC GGA TGG TTC GAC AGC GGA CTG GTG CCG	150
Gly Pro Asp Pro Pro Ala Ser Gly Trp Phe Asp Ser Gly Leu Val Pro	
25 30 35	
AGC AGG CCC ATC TGC GCG GCT TCC TCG TCG GCT GGG TTG CCG CCG CCG	198
Ser Arg Pro Ile Cys Ala Ala Ser Ser Ser Ala Gly Leu Pro Pro Pro	
40 45 50	
GTG CCG CCC ACC TGG CTG AAC AAC GAC GTC ACC TGC TGC AGC GGC TGG	246
Val Pro Pro Thr Trp Leu Asn Asn Asp Val Thr Cys Cys Ser Gly Trp	
55 60 65 70	
GTC AGC TGC TGC ATC GGG CCG CTC ATC TCA CCC AGT TGG CCG AGG GTC	294
Val Ser Cys Cys Ile Gly Pro Leu Ile Ser Pro Ser Trp Pro Arg Val	
75 80 85	
TGG GTA GCC GCC GGC GGC AAC TGG CCA ACC GGT GTT GAG CTG CCA GGG	342
Trp Val Ala Ala Gly Gly Asn Trp Pro Thr Gly Val Glu Leu Pro Gly	
90 95 100	
GAG GGC ATT CCG AAG ATC GGG TTC GTC GTG CTC TGG CTC GCG CCG GGA	390
Glu Gly Ile Pro Lys Ile Gly Phe Val Val Leu Trp Leu Ala Pro Gly	
105 110 115	
TCA AGG ATC GAC GCC ATC GGC TCG AGC TTC TCG AAA AGC GTG TTA ACC	438
Ser Arg Ile Asp Ala Ile Gly Ser Ser Phe Ser Lys Ser Val Leu Thr	
120 125 130	
GCG GTC TCG GCC TGG TAGACCT	460
Ala Val Ser Ala Trp	
135	

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

Met Arg Val Asn Asp Pro Pro Ala Pro Gly Ser Asp Ser Ala Arg Ser
 1             5             10             15

Arg Pro Ala Pro Ala Leu Gly Pro Asp Pro Pro Ala Ser Gly Trp Phe
          20             25             30

Asp Ser Gly Leu Val Pro Ser Arg Pro Ile Cys Ala Ala Ser Ser Ser
      35             40             45

Ala Gly Leu Pro Pro Pro Val Pro Pro Thr Trp Leu Asn Asn Asp Val
 50             55             60

Thr Cys Cys Ser Gly Trp Val Ser Cys Cys Ile Gly Pro Leu Ile Ser
 65             70             75             80

Pro Ser Trp Pro Arg Val Trp Val Ala Ala Gly Gly Asn Trp Pro Thr
          85             90             95

Gly Val Glu Leu Pro Gly Glu Gly Ile Pro Lys Ile Gly Phe Val Val
          100             105             110

Leu Trp Leu Ala Pro Gly Ser Arg Ile Asp Ala Ile Gly Ser Ser Phe
      115             120             125

Ser Lys Ser Val Leu Thr Ala Val Ser Ala Trp
      130             135

```

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 28...1140
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

TAATAGGCC	CCAACACATC	GGAGGGA	GTG	ATC	ACC	ATG	CTG	TGG	CAC	GCA	ATG	54
			Met	Ile	Thr	Met	Leu	Trp	His	Ala	Met	
			1				5					
CCA	CCG	GAG	CTA	AAT	ACC	GCA	CGG	CTG	ATG	GCC	GGC	102
Pro	Pro	Glu	Leu	Asn	Thr	Ala	Arg	Leu	Met	Ala	Gly	
10				15				20			25	
CCA	ATG	CTT	GCG	GCG	GCC	GCG	GGA	TGG	CAG	ACG	CTT	150
Pro	Met	Leu	Ala	Ala	Ala	Ala	Gly	Trp	Gln	Thr	Leu	
			30				35				40	
GAC	GCT	CAG	GCC	GTC	GAG	TTG	ACC	GCG	CGC	CTG	AAC	198
Asp	Ala	Gln	Ala	Val	Glu	Leu	Thr	Ala	Arg	Leu	Asn	
			45				50				55	
GCC	TGG	ACT	GGA	GGT	GGC	AGC	GAC	AAG	GCG	CTT	GCG	246
Ala	Trp	Thr	Gly	Gly	Gly	Ser	Asp	Lys	Ala	Leu	Ala	
			60			65					70	
ATG	GTG	GTC	TGG	CTA	CAA	ACC	GCG	TCA	ACA	CAG	GCC	294
Met	Val	Val	Trp	Leu	Gln	Thr	Ala	Ser	Thr	Gln	Ala	
	75				80					85		
ATG	CAG	GCG	ACG	GCG	CAA	GCC	GCG	GCA	TAC	ACC	CAG	342
Met	Gln	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Tyr	Thr	Gln	
	90				95				100		105	
ACG	CCG	TCG	CTG	CCG	GAG	ATC	GCC	GCC	AAC	CAC	ATC	390
Thr	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Ala	Asn	His	Ile	
				110					115			
CTT	ACG	GCC	ACC	AAC	TTC	TTC	GGT	ATC	AAC	ACG	ATC	438
Leu	Thr	Ala	Thr	Asn	Phe	Phe	Gly	Ile	Asn	Thr	Ile	
			125				130				135	
ACC	GAG	ATG	GAT	TAT	TTC	ATC	CGT	ATG	TGG	AAC	CAG	486
Thr	Glu	Met	Asp	Tyr	Phe	Ile	Arg	Met	Trp	Asn	Gln	
			140				145				150	
ATG	GAG	GTC	TAC	CAG	GCC	GAG	ACC	GCG	GTT	AAC	ACG	534
Met	Glu	Val	Tyr	Gln	Ala	Glu	Thr	Ala	Val	Asn	Thr	
	155				160					165		
CTC	GAG	CCG	ATG	GCG	TCG	ATC	CTT	GAT	CCC	GGC	GCG	582
Leu	Glu	Pro	Met	Ala	Ser	Ile	Leu	Asp	Pro	Gly	Ala	
	170			175						180		
ACG	AAC	CCG	ATC	TTC	GGA	ATG	CCC	TCC	CCT	GGC	AGC	630
Thr	Asn	Pro	Ile	Phe	Gly	Met	Pro	Ser	Pro	Gly	Ser	
				190					195			
GGC	CAG	TTG	CCG	CCG	GCG	GCT	ACC	CAG	ACC	CTC	GGC	678
Gly	Gln	Leu	Pro	Pro	Ala	Ala	Thr	Gln	Thr	Leu	Gly	
			205				210				215	
ATG	AGC	GGC	CCG	ATG	CAG	CAG	CTG	ACC	CAG	CCG	CTG	726
Met	Ser	Gly	Pro	Met	Gln	Gln	Leu	Thr	Gln	Pro	Leu	

200

220					225					230							
TCG	TTG	TTC	AGC	CAG	GTG	GGC	GGC	ACC	GGC	GGC	GGC	AAC	CCA	GCC	GAC	774	
Ser	Leu	Phe	Ser	Gln	Val	Gly	Gly	Thr	Gly	Gly	Gly	Asn	Pro	Ala	Asp		
235					240					245							
GAG	GAA	GCC	GCG	CAG	ATG	GGC	CTG	CTC	GGC	ACC	AGT	CCG	CTG	TCG	AAC	822	
Glu	Glu	Ala	Ala	Gln	Met	Gly	Leu	Leu	Gly	Thr	Ser	Pro	Leu	Ser	Asn		
250					255					260					265		
CAT	CCG	CTG	GCT	GGT	GGA	TCA	GGC	CCC	AGC	GCG	GGC	GCG	GGC	CTG	CTG	870	
His	Pro	Leu	Ala	Gly	Gly	Ser	Gly	Pro	Ser	Ala	Gly	Ala	Gly	Leu	Leu		
270					275					280							
CGC	GCG	GAG	TCG	CTA	CCT	GGC	GCA	GGT	GGG	TCG	TTG	ACC	CGC	ACG	CCG	918	
Arg	Ala	Glu	Ser	Leu	Pro	Gly	Ala	Gly	Gly	Ser	Leu	Thr	Arg	Thr	Pro		
285					290					295							
CTG	ATG	TCT	CAG	CTG	ATC	GAA	AAG	CCG	GTT	GCC	CCC	TCG	GTG	ATG	CCG	966	
Leu	Met	Ser	Gln	Leu	Ile	Glu	Lys	Pro	Val	Ala	Pro	Ser	Val	Met	Pro		
300					305					310							
GCG	GCT	GCT	GCC	GGA	TCG	TCG	GCG	ACG	GGT	GGC	GCC	GCT	CCG	GTG	GGT	1014	
Ala	Ala	Ala	Ala	Gly	Ser	Ser	Ala	Thr	Gly	Gly	Ala	Ala	Pro	Val	Gly		
315					320					325							
GCG	GGA	GCG	ATG	GGC	CAG	GGT	GCG	CAA	TCC	GGC	GGC	TCC	ACC	AGG	CCG	1062	
Ala	Gly	Ala	Met	Gly	Gln	Gly	Ala	Gln	Ser	Gly	Gly	Ser	Thr	Arg	Pro		
330					335					340					345		
GGT	CTG	GTC	GCG	CCG	GCA	CCG	CTC	GCG	CAG	GAG	CGT	GAA	GAA	GAC	GAC	1110	
Gly	Leu	Val	Ala	Pro	Ala	Pro	Leu	Ala	Gln	Glu	Arg	Glu	Glu	Asp	Asp		
350					355					360							
GAG	GAC	GAC	TGG	GAC	GAA	GAG	GAC	GAC	TGG	TGAGCTCCCG	TAATGACAAC	AGA				1163	
Glu	Asp	Asp	Trp	Asp	Glu	Glu	Asp	Asp	Trp								
365					370												
CTTCCCGGCC ACCCGGGCCG GAAGACTTGC CAACATT																1200	

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Met	Ile	Thr	Met	Leu	Trp	His	Ala	Met	Pro	Pro	Glu	Leu	Asn	Thr	Ala
1				5					10				15		
Arg Leu Met Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala															

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Ala Gln Ser Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro
 340 345 350

Leu Ala Gln Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu
 355 360 365

Asp Asp Trp
 370

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 46...969
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

GACGCGACAC AGAAATCCTT AAGGCCGGCG GCCAAGGGGC CGAAG GTG AAG AAG GTG	57
Met Lys Lys Val	
1	
AAG CCC CAG AAA CCG AAG GCC ACG AAG CCG CCC AAA GTG GTG TCG CAG	105
Lys Pro Gln Lys Pro Lys Ala Thr Lys Pro Pro Lys Val Val Ser Gln	
5 10 15 20	
CGC GGC TGG CGA CAT TGG GTG CAT GCG TTG ACG CGA ATC AAC CTG GGC	153
Arg Gly Trp Arg His Trp Val His Ala Leu Thr Arg Ile Asn Leu Gly	
25 30 35	
CTG TCA CCC GAC GAG AAG TAC GAG CTG GAC CTG CAC GCT CGA GTC CGC	201
Leu Ser Pro Asp Glu Lys Tyr Glu Leu Asp Leu His Ala Arg Val Arg	
40 45 50	
CGC AAT CCC CGC GGG TCG TAT CAG ATC GCC GTC GTC GGT CTC AAA GGT	249
Arg Asn Pro Arg Gly Ser Tyr Gln Ile Ala Val Val Gly Leu Lys Gly	
55 60 65	
GGG GCT GGC AAA ACC ACG CTG ACA GCA GCG TTG GGG TCG ACG TTG GCT	297
Gly Ala Gly Lys Thr Thr Leu Thr Ala Ala Leu Gly Ser Thr Leu Ala	
70 75 80	
CAG GTG CGG GCC GAC CGG ATC CTG GCT CTA GAC GCG GAT CCA GGC GCC	345
Gln Val Arg Ala Asp Arg Ile Leu Ala Leu Asp Ala Asp Pro Gly Ala	
85 90 95 100	
GGA AAC CTC GCC GAT CGG GTA GGG CGA CAA TCG GGC GCG ACC ATC GCT	393
Gly Asn Leu Ala Asp Arg Val Gly Arg Gln Ser Gly Ala Thr Ile Ala	
105 110 115	

203

GAT GTG CTT GCA GAA AAA GAG CTG TCG CAC TAC AAC GAC ATC CGC GCA Asp Val Leu Ala Glu Lys Glu Leu Ser His Tyr Asn Asp Ile Arg Ala 120 125 130	441
CAC ACT AGC GTC AAT GCG GTC AAT CTG GAA GTG CTG CCG GCA CCG GAA His Thr Ser Val Asn Ala Val Asn Leu Glu Val Leu Pro Ala Pro Glu 135 140 145	489
TAC AGC TCG GCG CAG CGC GCG CTC AGC GAC GCC GAC TGG CAT TTC ATC Tyr Ser Ser Ala Gln Arg Ala Leu Ser Asp Ala Asp Trp His Phe Ile 150 155 160	537
GCC GAT CCT GCG TCG AGG TTT TAC AAC CTC GTC TTG GCT GAT TGT GGG Ala Asp Pro Ala Ser Arg Phe Tyr Asn Leu Val Leu Ala Asp Cys Gly 165 170 175 180	585
GCC GGC TTC TTC GAC CCG CTG ACC CGC GGC GTG CTG TCC ACG GTG TCC Ala Gly Phe Phe Asp Pro Leu Thr Arg Gly Val Leu Ser Thr Val Ser 185 190 195	633
GGT GTC GTG GTC GTG GCA AGT GTC TCA ATC GAC GGC GCA CAA CAG GCG Gly Val Val Val Val Ala Ser Val Ser Ile Asp Gly Ala Gln Gln Ala 200 205 210	681
TCG GTC GCG TTG GAC TGG TTG CGC AAC AAC GGT TAC CAA GAT TTG GCG Ser Val Ala Leu Asp Trp Leu Arg Asn Asn Gly Tyr Gln Asp Leu Ala 215 220 225	729
AGC CGC GCA TGC GTG GTC ATC AAT CAC ATC ATG CCG GGA GAA CCC AAT Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro Gly Glu Pro Asn 230 235 240	777
GTC GCA GTT AAA GAC CTG GTG CGG CAT TTC GAA CAG CAA GTT CAA CCC Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln Gln Val Gln Pro 245 250 255 260	825
GGC CGG GTC GTG GTC ATG CCG TGG GAC AGG CAC ATT GCG GCC GGA ACC Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile Ala Ala Gly Thr 265 270 275	873
GAG ATT TCA CTC GAC TTG CTC GAC CCT ATC TAC AAG CGC AAG GTC CTC Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys Arg Lys Val Leu 280 285 290	921
GAA TTG GCC GCA GCG CTA TCC GAC GAT TTC GAG AGG GCT GGA CGT CGT T Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg Ala Gly Arg Arg 295 300 305	970
GAGCGCACCT GCTGTTGCTG CTGGTCCTAC	1000

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

Met Lys Lys Val Lys Pro Gln Lys Pro Lys Ala Thr Lys Pro Pro Lys
 1           5           10           15

Val Val Ser Gln Arg Gly Trp Arg His Trp Val His Ala Leu Thr Arg
          20           25           30

Ile Asn Leu Gly Leu Ser Pro Asp Glu Lys Tyr Glu Leu Asp Leu His
          35           40           45

Ala Arg Val Arg Arg Asn Pro Arg Gly Ser Tyr Gln Ile Ala Val Val
          50           55           60

Gly Leu Lys Gly Gly Ala Gly Lys Thr Thr Leu Thr Ala Ala Leu Gly
          65           70           75           80

Ser Thr Leu Ala Gln Val Arg Ala Asp Arg Ile Leu Ala Leu Asp Ala
          85           90           95

Asp Pro Gly Ala Gly Asn Leu Ala Asp Arg Val Gly Arg Gln Ser Gly
          100          105          110

Ala Thr Ile Ala Asp Val Leu Ala Glu Lys Glu Leu Ser His Tyr Asn
          115          120          125

Asp Ile Arg Ala His Thr Ser Val Asn Ala Val Asn Leu Glu Val Leu
          130          135          140

Pro Ala Pro Glu Tyr Ser Ser Ala Gln Arg Ala Leu Ser Asp Ala Asp
          145          150          155          160

Trp His Phe Ile Ala Asp Pro Ala Ser Arg Phe Tyr Asn Leu Val Leu
          165          170          175

Ala Asp Cys Gly Ala Gly Phe Phe Asp Pro Leu Thr Arg Gly Val Leu
          180          185          190

Ser Thr Val Ser Gly Val Val Val Val Ala Ser Val Ser Ile Asp Gly
          195          200          205

Ala Gln Gln Ala Ser Val Ala Leu Asp Trp Leu Arg Asn Asn Gly Tyr
          210          215          220

Gln Asp Leu Ala Ser Arg Ala Cys Val Val Ile Asn His Ile Met Pro
          225          230          235          240

Gly Glu Pro Asn Val Ala Val Lys Asp Leu Val Arg His Phe Glu Gln
          245          250          255

Gln Val Gln Pro Gly Arg Val Val Val Met Pro Trp Asp Arg His Ile
          260          265          270

Ala Ala Gly Thr Glu Ile Ser Leu Asp Leu Leu Asp Pro Ile Tyr Lys
          275          280          285

```

205

Arg Lys Val Leu Glu Leu Ala Ala Ala Leu Ser Asp Asp Phe Glu Arg
290 295 300

Ala Gly Arg Arg
305

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGAGTAGAT CTATGATGGC CGAGGATGTT CGCG

34

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CGGCGACGAC GGATCCTACC GCGTCGG

27

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCTTGGGAGA TCTTTGGACC CCGGTTGC

28

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

GACGAGATCT TATGGGCTTA CTGAC

25

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCCCCAGAT CTGCACCACC GGCATCGGCG GGC

33

(2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

GCGGCGGATC CGTTGCTTAG CCGG

24

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

CCGGCTGAGA TCTATGACAG AATACGAAGG GC

32

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

CCCCGCCAGG GAACTAGAGG CGGC

24

(2) INFORMATION FOR SEQ ID NO: 103:

207

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CTGCCGAGAT CTACCACCAT TGTCGCGCTG AAATACCC

38

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CGCCATGGCC TTACGCGCCA ACTCG

25

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGCGGAGATC TGTGAGTTTT CCGTATTTCA TC

32

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

CGCGTCGAGC CATGGTTAGG CGCAG

25

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GAGGAAGATC TATGACAACT TCACCCGACC CG

32

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CATGAAGCCA TGGCCCGCAG GCTGCATG

28

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GGCCGAGATC TGTGACCCAC TATGACGTCG TCG

33

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

GGCGCCCATG GTCAGAAATT GATCATGTGG CCAACC

36

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGGGAGATC TATGGCAAAG CTCTCCACCG ACG

33

(2) INFORMATION FOR SEQ ID NO: 112:

209

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CGCTGGGCAG AGCTACTTGA CGGTGACGGT GG

32

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

GGCCCAGATC TATGGCCATT GAGGTTTCGG TGTTCG

36

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CGCCGTGTTG CATGGCAGCG CTGAGC

26

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GGACGTTCAA GCGACACATC GCCG

24

(2) INFORMATION FOR SEQ ID NO: 116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CAGCACGAAC GCGCCGTCGA TGGC

24

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ACAGATCTGT GACGGACATG AACCCG

26

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

TTTTCCATGG TCACGGGCCC CCGGTACT

28

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ACAGATCTGT GCCCATGGCA CAGATA

26

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TTTAAGCTTC TAGGCGCCCA GCGCGGC

27

(2) INFORMATION FOR SEQ ID NO: 121:

211

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

ACAGATCTGC GCATGCGGAT CCGTGT

26

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TTTTCATGG TCATCCGGCG TGATCGAG

28

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

ACAGATCTGT AATGGCAGAC TGTGAT

26

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TTTTCATGG TCAGGAGATG GTGATCGA

28

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ACAGATCTGC CGGCTACCCC GGTGCC

26

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

TTTTCCATGG CTATTGCAGC TTTCCGGC

28

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val
 1 5 10 15

Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu
 20 25 30

Glu Ser Met Tyr Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr
 35 40 45

Val Ser
 50

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val
 1 5 10 15

Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu
 20 25 30

213

Glu Ser Met Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr Val
 35 40 45

Ser

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Ala Glu Asp Val Arg Ala Glu Ile Val Ala Ser Val Leu Glu Val Val
 1 5 10 15
 Val Asn Glu Gly Asp Gln Ile Asp Lys Gly Asp Val Val Val Leu Leu
 20 25 30
 Glu Ser Met Lys Met Glu Ile Pro Val Leu Ala Glu Ala Ala Gly Thr
 35 40 45
 Val Ser
 50

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

CCGGGAGATC TATGGCAAAG CTCTCCACCG ACG

33

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

CGCTGGGCAG AGCTACTTGA CGGTGACGGT GG

32

(2) INFORMATION FOR SEQ ID NO: 132:

214

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

GGCGCCGGCA AGCTTGCCAT GACAGAGCAG CAGTGG

36

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CGAACTCGCC GGATCCCGTG TTTCGC

26

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

GGCAACCGCG AGATCTTTCT CCCGGCCGGG GC

32

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

GGCAAGCTTG CCGGCGCCTA ACGAACT

27

(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

GGACCCAGAT CTATGACAGA GCAGCAGTGG

30

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CCGGCAGCCC CGGCCGGGAG AAAAGCTTTG CGAACATCCC AGTGACG

47

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

GTTTCGCAAAG CTTTTCTCCC GGCCGGGGCT GCCGGTCGAG TACC

44

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CCTTCGGTGG ATCCCGTCAG

20

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 68...346
- (D) OTHER INFORMATION:

216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

TGGCGCTGTC ACCGAGGAAC CTGTCAATGT CGTCGAGCAG TACTGAACCG TTCCGAGAAA      60
GGCCAGC  ATG  AAC  GTC  ACC  GTA  TCC  ATT  CCG  ACC  ATC  CTG  CGG  CCC  CAC      109
      Met Asn Val Thr Val Ser Ile Pro Thr Ile Leu Arg Pro His
          1              5              10
ACC  GGC  GGC  CAG  AAG  AGT  GTC  TCG  GCC  AGC  GGC  GAT  ACC  TTG  GGT  GCC      157
Thr  Gly  Gly  Gln  Lys  Ser  Val  Ser  Ala  Ser  Gly  Asp  Thr  Leu  Gly  Ala
      15              20              25              30
GTC  ATC  AGC  GAC  CTG  GAG  GCC  AAC  TAT  TCG  GGC  ATT  TCC  GAG  CGC  CTG      205
Val  Ile  Ser  Asp  Leu  Glu  Ala  Asn  Tyr  Ser  Gly  Ile  Ser  Glu  Arg  Leu
          35              40              45
ATG  GAC  CCG  TCT  TCC  CCA  GGT  AAG  TTG  CAC  CGC  TTC  GTG  AAC  ATC  TAC      253
Met  Asp  Pro  Ser  Ser  Pro  Gly  Lys  Leu  His  Arg  Phe  Val  Asn  Ile  Tyr
          50              55              60
GTC  AAC  GAC  GAG  GAC  GTG  CGG  TTC  TCC  GGC  GGC  TTG  GCC  ACC  GCG  ATC      301
Val  Asn  Asp  Glu  Asp  Val  Arg  Phe  Ser  Gly  Gly  Leu  Ala  Thr  Ala  Ile
          65              70              75
GCT  GAC  GGT  GAC  TCG  GTC  ACC  ATC  CTC  CCC  GCC  GTG  GCC  GGT  GGG  TGAGC      351
Ala  Asp  Gly  Asp  Ser  Val  Thr  Ile  Leu  Pro  Ala  Val  Ala  Gly  Gly
          80              85              90
GGAGCACATG ACACGATACG ACTCGCTGTT GCAGGCCTTG GGCAACACGC CGCTGGTTGG      411
CCTGCAGCGA TTGTCGCCAC GCTGGGATGA CGGGCGAGA      450

```

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

Met Asn Val Thr Val Ser Ile Pro Thr Ile Leu Arg Pro His Thr Gly
      1              5              10              15
Gly Gln Lys Ser Val Ser Ala Ser Gly Asp Thr Leu Gly Ala Val Ile
          20              25              30
Ser Asp Leu Glu Ala Asn Tyr Ser Gly Ile Ser Glu Arg Leu Met Asp
          35              40              45
Pro Ser Ser Pro Gly Lys Leu His Arg Phe Val Asn Ile Tyr Val Asn
          50              55              60

```

217

Asp Glu Asp Val Arg Phe Ser Gly Gly Leu Ala Thr Ala Ile Ala Asp
 65 70 75 80

Gly Asp Ser Val Thr Ile Leu Pro Ala Val Ala Gly Gly
 85 90

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 88...381
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

GGTGTTCCTCCG CGGCCGGCTA TGACAACAGT CAATGTGCAT GACAAGTTAC AGGTATTAGG      60
TCCAGGTTCA ACAAGGAGAC AGGCAAC ATG GCA ACA CGT TTT ATG ACG GAT CCG      114
Met Ala Thr Arg Phe Met Thr Asp Pro
      1                      5
CAC GCG ATG CGG GAC ATG GCG GGC CGT TTT GAG GTG CAC GCC CAG ACG      162
His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr
      10          15          20          25
GTG GAG GAC GAG GCT CGC CGG ATG TGG GCG TCC GCG CAA AAC ATC TCG      210
Val Glu Asp Glu Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser
      30          35          40
GGC GCG GGC TGG AGT GGC ATG GCC GAG GCG ACC TCG CTA GAC ACC ATG      258
Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met
      45          50          55
GCC CAG ATG AAT CAG GCG TTT CGC AAC ATC GTG AAC ATG CTG CAC GGG      306
Ala Gln Met Asn Gln Ala Phe Arg Asn Ile Val Asn Met Leu His Gly
      60          65          70
GTG CGT GAC GGG CTG GTT CGC GAC GCC AAC AAC TAC GAG CAG CAA GAG      354
Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu
      75          80          85
CAG GCC TCC CAG CAG ATC CTC AGC AGC TAACGTCAGC CGCTGCAGCA CAATACT      408
Gln Ala Ser Gln Gln Ile Leu Ser Ser
      90          95
TTTACAAGCG AAGGAGAACA GGTTTCGATGA CCATCAACTA TCAGTTCGGT GATGTCGACG      468
CTCATGGCGC CA      480

```

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(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

Met Ala Thr Arg Phe Met Thr Asp Pro His Ala Met Arg Asp Met Ala
 1             5             10             15
Gly Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
          20             25             30
Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met
          35             40             45
Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe
          50             55             60
Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly Leu Val Arg
          65             70             75             80
Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln Gln Ile Leu
          85             90             95
Ser Ser

```

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 86...868
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

GCCCCAGTCC TCGATCGCCT CATCGCCTTC ACCGGCCGCC AGCCGACCGC AGGCCACGTG      60
TCCGCCACCT AACGAAAGGA TGATC ATG CCC AAG AGA AGC GAA TAC AGG CAA      112
          Met Pro Lys Arg Ser Glu Tyr Arg Gln
          1             5
GGC ACG CCG AAC TGG GTC GAC CTT CAG ACC ACC GAT CAG TCC GCC GCC      160

```


219

Gly	Thr	Pro	Asn	Trp	Val	Asp	Leu	Gln	Thr	Thr	Asp	Gln	Ser	Ala	Ala		
10					15					20					25		
AAA	AAG	TTC	TAC	ACA	TCG	TTG	TTC	GGC	TGG	GGT	TAC	GAC	GAC	AAC	CCG		208
Lys	Lys	Phe	Tyr	Thr	Ser	Leu	Phe	Gly	Trp	Gly	Tyr	Asp	Asp	Asn	Pro		
				30					35					40			
GTC	CCC	GGA	GGC	GGT	GGG	GTC	TAT	TCC	ATG	GCC	ACG	CTG	AAC	GGC	GAA		256
Val	Pro	Gly	Gly	Gly	Gly	Val	Tyr	Ser	Met	Ala	Thr	Leu	Asn	Gly	Glu		
			45					50					55				
GCC	GTG	GCC	GCC	ATC	GCA	CCG	ATG	CCC	CCG	GGT	GCA	CCG	GAG	GGG	ATG		304
Ala	Val	Ala	Ala	Ile	Ala	Pro	Met	Pro	Pro	Gly	Ala	Pro	Glu	Gly	Met		
			60				65					70					
CCG	CCG	ATC	TGG	AAC	ACC	TAT	ATC	GCG	GTG	GAC	GAC	GTC	GAT	GCG	GTG		352
Pro	Pro	Ile	Trp	Asn	Thr	Tyr	Ile	Ala	Val	Asp	Asp	Val	Asp	Ala	Val		
	75					80					85						
GTG	GAC	AAG	GTG	GTG	CCC	GGG	GGC	GGG	CAG	GTG	ATG	ATG	CCG	GCC	TTC		400
Val	Asp	Lys	Val	Val	Pro	Gly	Gly	Gly	Gln	Val	Met	Met	Pro	Ala	Phe		
90					95				100						105		
GAC	ATC	GGC	GAT	GCC	GGC	CGG	ATG	TCG	TTC	ATC	ACC	GAT	CCG	ACC	GGC		448
Asp	Ile	Gly	Asp	Ala	Gly	Arg	Met	Ser	Phe	Ile	Thr	Asp	Pro	Thr	Gly		
				110					115					120			
GCT	GCC	GTG	GGC	CTA	TGG	CAG	GCC	AAT	CGG	CAC	ATC	GGA	GCG	ACG	TTG		496
Ala	Ala	Val	Gly	Leu	Trp	Gln	Ala	Asn	Arg	His	Ile	Gly	Ala	Thr	Leu		
			125					130					135				
GTC	AAC	GAG	ACG	GGC	ACG	CTC	ATC	TGG	AAC	GAA	CTG	CTC	ACG	GAC	AAG		544
Val	Asn	Glu	Thr	Gly	Thr	Leu	Ile	Trp	Asn	Glu	Leu	Leu	Thr	Asp	Lys		
		140					145					150					
CCG	GAT	TTG	GCG	CTA	GCG	TTC	TAC	GAG	GCT	GTG	GTT	GGC	CTC	ACC	CAC		592
Pro	Asp	Leu	Ala	Leu	Ala	Phe	Tyr	Glu	Ala	Val	Val	Gly	Leu	Thr	His		
	155					160					165						
TCG	AGC	ATG	GAG	ATA	GCT	GCG	GGC	CAG	AAC	TAT	CGG	GTG	CTC	AAG	GCC		640
Ser	Ser	Met	Glu	Ile	Ala	Ala	Gly	Gln	Asn	Tyr	Arg	Val	Leu	Lys	Ala		
170					175				180						185		
GGC	GAC	GCG	GAA	GTC	GGC	GGC	TGT	ATG	GAA	CCG	CCG	ATG	CCC	GGC	GTG		688
Gly	Asp	Ala	Glu	Val	Gly	Gly	Cys	Met	Glu	Pro	Pro	Met	Pro	Gly	Val		
				190					195					200			
CCG	AAT	CAT	TGG	CAC	GTC	TAC	TTT	GCG	GTG	GAT	GAC	GCC	GAC	GCC	ACG		736
Pro	Asn	His	Trp	His	Val	Tyr	Phe	Ala	Val	Asp	Asp	Ala	Asp	Ala	Thr		
			205					210					215				
GCG	GCC	AAA	GCC	GCC	GCA	GCG	GGC	GGC	CAG	GTC	ATT	GCG	GAA	CCG	GCT		784
Ala	Ala	Lys	Ala	Ala	Ala	Ala	Gly	Gly	Gln	Val	Ile	Ala	Glu	Pro	Ala		
		220					225					230					
GAC	ATT	CCG	TCG	GTG	GGC	CGG	TTC	GCC	GTG	TTG	TCC	GAT	CCG	CAG	GGC		832
Asp	Ile	Pro	Ser	Val	Gly	Arg	Phe	Ala	Val	Leu	Ser	Asp	Pro	Gln	Gly		
	235					240					245						

GCG ATC TTC AGT GTG TTG AAG CCC GCA CCG CAG CAA TAGGGAGCAT CCCGGG 884
 Ala Ile Phe Ser Val Leu Lys Pro Ala Pro Gln Gln
 250 255 260

CAGGCCCGCC GGCCGGCAGA TTCGGAGAAT GCTAGAAGCT GCCGCCGGCG CCGCCG 940

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

Met	Pro	Lys	Arg	Ser	Glu	Tyr	Arg	Gln	Gly	Thr	Pro	Asn	Trp	Val	Asp	1	5	10	15
Leu	Gln	Thr	Thr	Asp	Gln	Ser	Ala	Ala	Lys	Lys	Phe	Tyr	Thr	Ser	Leu	20	25	30	
Phe	Gly	Trp	Gly	Tyr	Asp	Asp	Asn	Pro	Val	Pro	Gly	Gly	Gly	Gly	Val	35	40	45	
Tyr	Ser	Met	Ala	Thr	Leu	Asn	Gly	Glu	Ala	Val	Ala	Ala	Ile	Ala	Pro	50	55	60	
Met	Pro	Pro	Gly	Ala	Pro	Glu	Gly	Met	Pro	Pro	Ile	Trp	Asn	Thr	Tyr	65	70	75	80
Ile	Ala	Val	Asp	Asp	Val	Asp	Ala	Val	Val	Asp	Lys	Val	Val	Pro	Gly	85	90	95	
Gly	Gly	Gln	Val	Met	Met	Pro	Ala	Phe	Asp	Ile	Gly	Asp	Ala	Gly	Arg	100	105	110	
Met	Ser	Phe	Ile	Thr	Asp	Pro	Thr	Gly	Ala	Ala	Val	Gly	Leu	Trp	Gln	115	120	125	
Ala	Asn	Arg	His	Ile	Gly	Ala	Thr	Leu	Val	Asn	Glu	Thr	Gly	Thr	Leu	130	135	140	
Ile	Trp	Asn	Glu	Leu	Leu	Thr	Asp	Lys	Pro	Asp	Leu	Ala	Leu	Ala	Phe	145	150	155	160
Tyr	Glu	Ala	Val	Val	Gly	Leu	Thr	His	Ser	Ser	Met	Glu	Ile	Ala	Ala	165	170	175	
Gly	Gln	Asn	Tyr	Arg	Val	Leu	Lys	Ala	Gly	Asp	Ala	Glu	Val	Gly	Gly	180	185	190	
Cys	Met	Glu	Pro	Pro	Met	Pro	Gly	Val	Pro	Asn	His	Trp	His	Val	Tyr	195	200	205	

221

Phe Ala Val Asp Asp Ala Asp Ala Thr Ala Ala Lys Ala Ala Ala Ala
 210 215 220

Gly Gly Gln Val Ile Ala Glu Pro Ala Asp Ile Pro Ser Val Gly Arg
 225 230 235 240

Phe Ala Val Leu Ser Asp Pro Gln Gly Ala Ile Phe Ser Val Leu Lys
 245 250 255

Pro Ala Pro Gln Gln
 260

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 47...247
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

CCGAAAGGCG GTGCACCGCA CCCAGAAGAA AAGGAAAGAT CGAGAA ATG CCA CAG 55
 Met Pro Gln
 1

GGA ACT GTG AAG TGG TTC AAC GCG GAG AAG GGG TTC GGC TTT ATC GCC 103
 Gly Thr Val Lys Trp Phe Asn Ala Glu Lys Gly Phe Gly Phe Ile Ala
 5 10 15

CCC GAA GAC GGT TCC GCG GAT GTA TTT GTC CAC TAC ACG GAG ATC CAG 151
 Pro Glu Asp Gly Ser Ala Asp Val Phe Val His Tyr Thr Glu Ile Gln
 20 25 30 35

GGA ACG GGC TTC CGC ACC CTT GAA GAA AAC CAG AAG GTC GAG TTC GAG 199
 Gly Thr Gly Phe Arg Thr Leu Glu Glu Asn Gln Lys Val Glu Phe Glu
 40 45 50

ATC GGC CAC AGC CCT AAG GGC CCC CAG GCC ACC GGA GTC CGC TCG CTC T 248
 Ile Gly His Ser Pro Lys Gly Pro Gln Ala Thr Gly Val Arg Ser Leu
 55 60 65

GAGTTACCCC CGCGAGCAGA CGCAAAAAGC CC 280

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

222

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

Met Pro Gln Gly Thr Val Lys Trp Phe Asn Ala Glu Lys Gly Phe Gly
 1             5             10             15
Phe Ile Ala Pro Glu Asp Gly Ser Ala Asp Val Phe Val His Tyr Thr
          20             25             30
Glu Ile Gln Gly Thr Gly Phe Arg Thr Leu Glu Glu Asn Gln Lys Val
          35             40             45
Glu Phe Glu Ile Gly His Ser Pro Lys Gly Pro Gln Ala Thr Gly Val
          50             55             60
Arg Ser Leu
65

```

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 105...491
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

ATCGTGTTCGT ATCGAGAACC CCGGCCGGTA TCAGAACGCG CCAGAGCGCA AACCTTTATA      60
ACTTCGTGTC CCAAATGTGA CGACCATGGA CCAAGGTTCC TGAG ATG AAC CTA CGG      116
                                     Met Asn Leu Arg
                                     1
CGC CAT CAG ACC CTG ACG CTG CGA CTG CTG GCG GCA TCC GCG GGC ATT      164
Arg His Gln Thr Leu Thr Leu Arg Leu Leu Ala Ala Ser Ala Gly Ile
 5             10             15             20
CTC AGC GCC GCG GCC TTC GCC GCG CCA GCA CAG GCA AAC CCC GTC GAC      212
Leu Ser Ala Ala Ala Phe Ala Ala Pro Ala Gln Ala Asn Pro Val Asp
          25             30             35
GAC GCG TTC ATC GCC GCG CTG AAC AAT GCC GGC GTC AAC TAC GGC GAT      260
Asp Ala Phe Ile Ala Ala Leu Asn Asn Ala Gly Val Asn Tyr Gly Asp
          40             45             50
CCG GTC GAC GCC AAA GCG CTG GGT CAG TCC GTC TGC CCG ATC CTG GCC      308
Pro Val Asp Ala Lys Ala Leu Gly Gln Ser Val Cys Pro Ile Leu Ala
          55             60             65

```

223

GAG CCC GGC GGG TCG TTT AAC ACC GCG GTA GCC AGC GTT GTG GCG CGC 356
 Glu Pro Gly Gly Ser Phe Asn Thr Ala Val Ala Ser Val Val Ala Arg
 70 75 80

GCC CAA GGC ATG TCC CAG GAC ATG GCG CAA ACC TTC ACC AGT ATC GCG 404
 Ala Gln Gly Met Ser Gln Asp Met Ala Gln Thr Phe Thr Ser Ile Ala
 85 90 95 100

ATT TCG ATG TAC TGC CCC TCG GTG ATG GCA GAC GTC GCC AGC GGC AAC 452
 Ile Ser Met Tyr Cys Pro Ser Val Met Ala Asp Val Ala Ser Gly Asn
 105 110 115

CTG CCG GCC CTG CCA GAC ATG CCG GGG CTG CCC GGG TCC TAGGCGTGCG CG 503
 Leu Pro Ala Leu Pro Asp Met Pro Gly Leu Pro Gly Ser
 120 125

GCTCCTAGCC GGTCCCTAAC GGATCGATCG TGGATGC 540

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Met Asn Leu Arg Arg His Gln Thr Leu Thr Leu Arg Leu Leu Ala Ala
 1 5 10 15

Ser Ala Gly Ile Leu Ser Ala Ala Ala Phe Ala Ala Pro Ala Gln Ala
 20 25 30

Asn Pro Val Asp Asp Ala Phe Ile Ala Ala Leu Asn Asn Ala Gly Val
 35 40 45

Asn Tyr Gly Asp Pro Val Asp Ala Lys Ala Leu Gly Gln Ser Val Cys
 50 55 60

Pro Ile Leu Ala Glu Pro Gly Gly Ser Phe Asn Thr Ala Val Ala Ser
 65 70 75 80

Val Val Ala Arg Ala Gln Gly Met Ser Gln Asp Met Ala Gln Thr Phe
 85 90 95

Thr Ser Ile Ala Ile Ser Met Tyr Cys Pro Ser Val Met Ala Asp Val
 100 105 110

Ala Ser Gly Asn Leu Pro Ala Leu Pro Asp Met Pro Gly Leu Pro Gly
 115 120 125

Ser

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 25...354
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 109..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

ATAGTTTGGG GAAGGTGTCC ATAA ATG AGG CTG TCG TTG ACC GCA TTG AGC	51
Met Arg Leu Ser Leu Thr Ala Leu Ser	
-28 -25 -20	
GCC GGT GTA GGC GCC GTG GCA ATG TCG TTG ACC GTC GGG GCC GGG GTC	99
Ala Gly Val Gly Ala Val Ala Met Ser Leu Thr Val Gly Ala Gly Val	
-15 -10 -5	
GCC TCC GCA GAT CCC GTG GAC GCG GTC ATT AAC ACC ACC TGC AAT TAC	147
Ala Ser Ala Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr	
1 5 10	
GGG CAG GTA GTA GCT GCG CTC AAC GCG ACG GAT CCG GGG GCT GCC GCA	195
Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala	
15 20 25	
CAG TTC AAC GCC TCA CCG GTG GCG CAG TCC TAT TTG CGC AAT TTC CTC	243
Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu	
30 35 40 45	
GCC GCA CCG CCA CCT CAG CGC GCT GCC ATG GCC GCG CAA TTG CAA GCT	291
Ala Ala Pro Pro Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala	
50 55 60	
GTG CCG GGG GCG GCA CAG TAC ATC GGC CTT GTC GAG TCG GTT GCC GGC	339
Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly	
65 70 75	
TCC TGC AAC AAC TAT TAAGCCCATG CGGGCCCCAT CCCGCGACCC GGCATCGTCG	394
Ser Cys Asn Asn Tyr	
80	
CCGGGG	400

(2) INFORMATION FOR SEQ ID NO: 151:

225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

Met Arg Leu Ser Leu Thr Ala Leu Ser Ala Gly Val Gly Ala Val Ala
-28          -25          -20          -15

Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro Val Asp
      -10          -5          1

Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu
  5          10          15          20

Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val
      25          30          35

Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg
      40          45          50

Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr
      55          60          65

Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
      70          75          80

```

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 93...890
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

AATAGTAATA TCGCTGTGCG GTTGCAAAC GTGTGACCGA GGTTCGCAG TCGAGCGCTG      60
CGGGCCGCCT TCGAGGAGGA CGAACCACAG TC ATG ACG AAC ATC GTG GTC CTG      113
                               Met Thr Asn Ile Val Val Leu
                               1          5

ATC AAG CAG GTC CCA GAT ACC TGG TCG GAG CGC AAG CTG ACC GAC GGC      161
Ile Lys Gln Val Pro Asp Thr Trp Ser Glu Arg Lys Leu Thr Asp Gly
      10          15          20

GAT TTC ACG CTG GAC CGC GAG GCC GCC GAC GCG GTG CTG GAC GAG ATC      209

```

226

Asp Phe Thr Leu Asp Arg Glu Ala Ala Asp Ala Val Leu Asp Glu Ile	
25 30 35	
AAC GAG CGC GCC GTG GAG GAA GCG CTA CAG ATT CGG GAG AAA GAG GCC	257
Asn Glu Arg Ala Val Glu Glu Ala Leu Gln Ile Arg Glu Lys Glu Ala	
40 45 50 55	
GCC GAC GGC ATC GAA GGG TCG GTA ACC GTG CTG ACG GCG GGC CCC GAG	305
Ala Asp Gly Ile Glu Gly Ser Val Thr Val Leu Thr Ala Gly Pro Glu	
60 65 70	
CGC GCC ACC GAG GCG ATC CGC AAG GCG CTG TCG ATG GGT GCC GAC AAG	353
Arg Ala Thr Glu Ala Ile Arg Lys Ala Leu Ser Met Gly Ala Asp Lys	
75 80 85	
GCC GTC CAC CTA AAG GAC GAC GGC ATG CAC GGC TCG GAC GTC ATC CAA	401
Ala Val His Leu Lys Asp Asp Gly Met His Gly Ser Asp Val Ile Gln	
90 95 100	
ACC GGG TGG GCT TTG GCG CGC GCG TTG GGC ACC ATC GAG GGC ACC GAG	449
Thr Gly Trp Ala Leu Ala Arg Ala Leu Gly Thr Ile Glu Gly Thr Glu	
105 110 115	
CTG GTG ATC GCA GGC AAC GAA TCG ACC GAC GGG GTG GGC GGT GCG GTG	497
Leu Val Ile Ala Gly Asn Glu Ser Thr Asp Gly Val Gly Gly Ala Val	
120 125 130 135	
CCG GCC ATC ATC GCC GAG TAC CTG GGC CTG CCG CAG CTC ACC CAC CTG	545
Pro Ala Ile Ile Ala Glu Tyr Leu Gly Leu Pro Gln Leu Thr His Leu	
140 145 150	
CGC AAA GTG TCG ATC GAG GGC GGC AAG ATC ACC GGC GAG CGT GAG ACC	593
Arg Lys Val Ser Ile Glu Gly Gly Lys Ile Thr Gly Glu Arg Glu Thr	
155 160 165	
GAT GAG GGC GTA TTC ACC CTC GAG GCC ACG CTG CCC GCG GTG ATC AGC	641
Asp Glu Gly Val Phe Thr Leu Glu Ala Thr Leu Pro Ala Val Ile Ser	
170 175 180	
GTG AAC GAG AAG ATC AAC GAG CCG CGC TTC CCG TCC TTC AAA GGC ATC	689
Val Asn Glu Lys Ile Asn Glu Pro Arg Phe Pro Ser Phe Lys Gly Ile	
185 190 195	
ATG GCC GCC AAG AAG AAG GAA GTT ACC GTG CTG ACC CTG GCC GAG ATC	737
Met Ala Ala Lys Lys Lys Glu Val Thr Val Leu Thr Leu Ala Glu Ile	
200 205 210 215	
GGT GTC GAG AGC GAC GAG GTG GGG CTG GCC AAC GCC GGA TCC ACC GTG	785
Gly Val Glu Ser Asp Glu Val Gly Leu Ala Asn Ala Gly Ser Thr Val	
220 225 230	
CTG GCG TCG ACG CCC AAA CCG GCC AAG ACT GCC GGG GAG AAG GTC ACC	833
Leu Ala Ser Thr Pro Lys Pro Ala Lys Thr Ala Gly Glu Lys Val Thr	
235 240 245	
GAC GAG GGT GAA GGC GGC AAC CAG ATC GTG CAG TAC CTG GTT GCC CAG	881
Asp Glu Gly Glu Gly Gly Asn Gln Ile Val Gln Tyr Leu Val Ala Gln	
250 255 260	

227

AAA ATC ATC TAAGACATAC GCACCTCCCA AAGACGAGAG CGATATAACC CATGGCTGA 939
 Lys Ile Ile
 265

AGTACTGGTG CTCGTTGAGC ACGCTGAAGG CGCGTTAAAG AAGGTCAGCG C 990

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Met	Thr	Asn	Ile	Val	Val	Leu	Ile	Lys	Gln	Val	Pro	Asp	Thr	Trp	Ser	
1				5					10					15		
Glu	Arg	Lys	Leu	Thr	Asp	Gly	Asp	Phe	Thr	Leu	Asp	Arg	Glu	Ala	Ala	
			20					25					30			
Asp	Ala	Val	Leu	Asp	Glu	Ile	Asn	Glu	Arg	Ala	Val	Glu	Glu	Ala	Leu	
			35				40					45				
Gln	Ile	Arg	Glu	Lys	Glu	Ala	Ala	Asp	Gly	Ile	Glu	Gly	Ser	Val	Thr	
	50					55					60					
Val	Leu	Thr	Ala	Gly	Pro	Glu	Arg	Ala	Thr	Glu	Ala	Ile	Arg	Lys	Ala	
	65				70				75						80	
Leu	Ser	Met	Gly	Ala	Asp	Lys	Ala	Val	His	Leu	Lys	Asp	Asp	Gly	Met	
			85					90						95		
His	Gly	Ser	Asp	Val	Ile	Gln	Thr	Gly	Trp	Ala	Leu	Ala	Arg	Ala	Leu	
			100					105					110			
Gly	Thr	Ile	Glu	Gly	Thr	Glu	Leu	Val	Ile	Ala	Gly	Asn	Glu	Ser	Thr	
		115				120						125				
Asp	Gly	Val	Gly	Gly	Ala	Val	Pro	Ala	Ile	Ile	Ala	Glu	Tyr	Leu	Gly	
			130			135					140					
Leu	Pro	Gln	Leu	Thr	His	Leu	Arg	Lys	Val	Ser	Ile	Glu	Gly	Gly	Lys	
			145		150					155				160		
Ile	Thr	Gly	Glu	Arg	Glu	Thr	Asp	Glu	Gly	Val	Phe	Thr	Leu	Glu	Ala	
			165					170					175			
Thr	Leu	Pro	Ala	Val	Ile	Ser	Val	Asn	Glu	Lys	Ile	Asn	Glu	Pro	Arg	
			180				185					190				
Phe	Pro	Ser	Phe	Lys	Gly	Ile	Met	Ala	Ala	Lys	Lys	Lys	Glu	Val	Thr	
			195				200					205				
Val	Leu	Thr	Leu	Ala	Glu	Ile	Gly	Val	Glu	Ser	Asp	Glu	Val	Gly	Leu	

228

210		215		220
Ala Asn Ala Gly Ser Thr Val Leu Ala Ser Thr Pro Lys Pro Ala Lys				
225		230		235
Thr Ala Gly Glu Lys Val Thr Asp Glu Gly Glu Gly Gly Asn Gln Ile				
	245		250	255
Val Gln Tyr Leu Val Ala Gln Lys Ile Ile				
	260		265	

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

CTGAGATCTA TGAACCTACG GCGCC

25

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

CTCCCATGGT ACCCTAGGAC CCGGGCAGCC CCGGC

35

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

CTGAGATCTA TGAGGCTGTC GTTGACCGC

29

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CTCCCCGGGC TTAATAGTTG TTGCAGGAGC

30

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GCTTAGATCT ATGATTTTCT GGGCAACCAG GTA

33

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

GCTTCCATGG GCGAGGCACA GGCGTGGGAA

30

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CTGAGATCTA GAATGCCACA GGGAACGTG

30

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

TCTCCCGGGG GTAAC TCAGA GCGAGCGGAC

30

(2) INFORMATION FOR SEQ ID NO: 162:

230

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CTGAGATCTA TGAACGTCAC CGTATCC

27

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TCTCCCGGGG CTCACCCACC GGCCACG

27

(2) INFORMATION FOR SEQ ID NO: 164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CTGAGATCTA TGGCAACACG TTTTATGACG

30

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CTCCCCGGGT TAGCTGCTGA GGATCTGCTH

30

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

CTGAAGATCT ATGCCCAAGA GAAGCGAATA C

31

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CGGCAGCTGC TAGCATTCTC CGAATCTGCC G

31

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Pro	Gln	Gly	Thr	Val	Lys	Trp	Phe	Asn	Ala	Glu	Lys	Gly	Phe	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 15
- (D) OTHER INFORMATION: Xaa is unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Asn	Val	Thr	Val	Ser	Ile	Pro	Thr	Ile	Leu	Arg	Pro	Xaa	Xaa	Xaa
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

232

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1

(D) OTHER INFORMATION: Thr Could also be Ala

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Thr	Arg	Phe	Met	Thr	Asp	Pro	His	Ala	Met	Arg	Asp	Met	Ala	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Pro	Lys	Arg	Ser	Glu	Tyr	Arg	Gln	Gly	Thr	Pro	Asn	Trp	Val	Asp
1		5				10			15					

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Ala	Thr	Val	Asn	Arg	Ser	Arg	His	His	His	His	His	His	His
1				5				10					15	
Ile	Glu	Gly	Arg	Ser	Phe	Ser	Arg	Pro	Gly	Leu	Pro	Val	Glu	Tyr
			20					25					30	
Gln	Val	Pro	Ser	Pro	Ser	Met	Gly	Arg	Asp	Ile	Lys	Val	Gln	Phe
			35				40					45		
Ser	Gly	Gly	Asn	Asn	Ser	Pro	Ala	Val	Tyr	Leu	Leu	Asp	Gly	Leu
			50			55					60			
Ala	Gln	Asp	Asp	Tyr	Asn	Gly	Trp	Asp	Ile	Asn	Thr	Pro	Ala	Phe
65					70				75					80
Trp	Tyr	Tyr	Gln	Ser	Gly	Leu	Ser	Ile	Val	Met	Pro	Val	Gly	Gly
			85					90					95	
Ser	Ser	Phe	Tyr	Ser	Asp	Trp	Tyr	Ser	Pro	Ala	Cys	Gly	Lys	Ala
			100					105					110	
Cys	Gln	Thr	Tyr	Lys	Trp	Glu	Thr	Phe	Leu	Thr	Ser	Glu	Leu	Pro
			115				120					125		
Trp	Leu	Ser	Ala	Asn	Arg	Ala	Val	Lys	Pro	Thr	Gly	Ser	Ala	Ile

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130		135		140											
Gly	Leu	Ser	Met	Ala	Gly	Ser	Ser	Ala	Met	Ile	Leu	Ala	Ala	Tyr	His
145		150		155		160									
Pro	Gln	Gln	Phe	Ile	Tyr	Ala	Gly	Ser	Leu	Ser	Ala	Leu	Leu	Asp	Pro
		165		170		175									
Ser	Gln	Gly	Met	Gly	Pro	Ser	Leu	Ile	Gly	Leu	Ala	Met	Gly	Asp	Ala
		180		185		190									
Gly	Gly	Tyr	Lys	Ala	Ala	Asp	Met	Trp	Gly	Pro	Ser	Ser	Asp	Pro	Ala
		195		200		205									
Trp	Glu	Arg	Asn	Asp	Pro	Thr	Gln	Gln	Ile	Pro	Lys	Leu	Val	Ala	Asn
		210		215		220									
Asn	Thr	Arg	Leu	Trp	Val	Tyr	Cys	Gly	Asn	Gly	Thr	Pro	Asn	Glu	Leu
		225		230		235									
Gly	Gly	Ala	Asn	Ile	Pro	Ala	Glu	Phe	Leu	Glu	Asn	Phe	Val	Arg	Ser
		245		250		255									
Ser	Asn	Leu	Lys	Phe	Gln	Asp	Ala	Tyr	Asn	Ala	Ala	Gly	Gly	His	Asn
		260		265		270									
Ala	Val	Phe	Asn	Phe	Pro	Pro	Asn	Gly	Thr	His	Ser	Trp	Glu	Tyr	Trp
		275		280		285									
Gly	Ala	Gln	Leu	Asn	Ala	Met	Lys	Gly	Asp	Leu	Gln	Ser	Ser	Leu	Gly
		290		295		300									
Ala	Gly	Lys	Leu	Ala	Met	Thr	Glu	Gln	Gln	Trp	Asn	Phe	Ala	Gly	Ile
		305		310		315									
Glu	Ala	Ala	Ala	Ser	Ala	Ile	Gln	Gly	Asn	Val	Thr	Ser	Ile	His	Ser
		325		330		335									
Leu	Leu	Asp	Glu	Gly	Lys	Gln	Ser	Leu	Thr	Lys	Leu	Ala	Ala	Ala	Trp
		340		345		350									
Gly	Gly	Ser	Gly	Ser	Glu	Ala	Tyr	Gln	Gly	Val	Gln	Gln	Lys	Trp	Asp
		355		360		365									
Ala	Thr	Ala	Thr	Glu	Leu	Asn	Asn	Ala	Leu	Gln	Asn	Leu	Ala	Arg	Thr
		370		375		380									
Ile	Ser	Glu	Ala	Gly	Gln	Ala	Met	Ala	Ser	Thr	Glu	Gly	Asn	Val	Thr
		385		390		395									
Gly	Met	Phe	Ala												

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Met	Ala	Thr	Val	Asn	Arg	Ser	Arg	His	His	His	His	His	His	His	His
1			5					10					15		
Ile	Glu	Gly	Arg	Ser	Met	Thr	Glu	Gln	Gln	Trp	Asn	Phe	Ala	Gly	Ile
		20					25						30		
Glu	Ala	Ala	Ala	Ser	Ala	Ile	Gln	Gly	Asn	Val	Thr	Ser	Ile	His	Ser
		35				40					45				
Leu	Leu	Asp	Glu	Gly	Lys	Gln	Ser	Leu	Thr	Lys	Leu	Ala	Ala	Ala	Trp
		50			55					60					
Gly	Gly	Ser	Gly	Ser	Glu	Ala	Tyr	Gln	Gly	Val	Gln	Gln	Lys	Trp	Asp
		65			70			75					80		
Ala	Thr	Ala	Thr	Glu	Leu	Asn	Asn	Ala	Leu	Gln	Asn	Leu	Ala	Arg	Thr

BNSDOCID: <WO__ 9844119A1 I_>

CLAIMS

1. A substantially pure polypeptide fragment which

- 5 a) comprises an amino acid sequence selected from the sequences shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 16, 17-23, 42, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72-86, 88, 90, 92, 94, 141, 143, 145, 147, 149, 151, 153, and 168-171,
- 10 b) comprises a subsequence of the polypeptide fragment defined in a) which has a length of at least 6 amino acid residues, said subsequence being immunologically equivalent to the polypeptide defined in a) with respect to the ability of evoking a protective immune response against infections with mycobacteria belonging to the tuberculosis complex or with respect to the
- 15 ability of eliciting a diagnostically significant immune response indicating previous or ongoing sensitization with antigens derived from mycobacteria belonging to the tuberculosis complex, or
- 20 c) comprises an amino acid sequence having a sequence identity with the polypeptide defined in a) or the subsequence defined in b) of at least 70% and at the same time being immunologically equivalent to the polypeptide defined in a) with respect to the ability of evoking a protective immune response against infections with mycobacteria belonging to the tuberculosis
- 25 complex or with respect to the ability of eliciting a diagnostically significant immune response indicating previous or ongoing sensitization with antigens derived from mycobacteria belonging to the tuberculosis complex,
- 30

with the proviso that

- i) the polypeptide fragment is in essentially pure form when consisting of the amino acid sequence 1-96 of SEQ ID NO: 2 or when consisting of the amino acid sequence 87-108 of SEQ ID NO: 4 fused to β -galactosidase,
- 5 ii) the degree of sequence identity in c) is at least 95% when the polypeptide comprises a homologue of a polypeptide which has the amino acid sequence SEQ ID NO: 12 or a subsequence thereof as defined in b), and
- 10 iii) the polypeptide fragment contains a threonine residue corresponding to position 213 in SEQ ID NO: 42 when comprising an amino acid sequence of at least 6 amino acids in SEQ ID NO: 42.
2. The polypeptide fragment according to claim 1 in essentially pure form.
- 15 3. The polypeptide fragment according to claim 1 or 2, which comprises an epitope for a T-helper cell.
4. The polypeptide fragment according to any of the preceding claims, which has a length of at least 7 amino acid residues, such as at least 8, at least 9, at least 10, at least 12, at
20 least 14, at least 16, at least 18, at least 20, at least 22, at least 24, and at least 30 amino acid residues.
5. The polypeptide fragment according to any of the preceding claims, which is free from amino acid residues -30 to -1 in SEQ ID NO: 6 and/or -32 to -1 in SEQ ID NO: 10 and/or -8 to
25 -1 in SEQ ID NO: 12 and/or -32 to -1 in SEQ ID NO: 14 and/or -33 to -1 in SEQ ID NO: 42 and/or -38 to -1 in SEQ ID NO: 52, and/or -33 to -1 in SEQ ID NO: 56 and/or -56 to -1 in SEQ ID NO: 58 and/or -28 to -1 in SEQ ID NO: 151.
6. The polypeptide fragment according to any of the preceding
30 claims which is free from any signal sequence.

7. The polypeptide fragment according to any of the preceding claims which

- 1) induces a release of IFN- γ from primed memory T-lymphocytes withdrawn from a mouse within 2 weeks of primary infection or within 4 days after the mouse has been re-challenge infected with mycobacteria belonging to the tuberculosis complex, the induction performed by the addition of the polypeptide to a suspension comprising about 200.000 spleen cells per ml, the addition of the polypeptide resulting in a concentration of 1-4 μ g polypeptide per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 2 days after the addition of the polypeptide to the suspension, and/or
- 2) induces a release of IFN- γ of at least 300 pg above background level from about 1000,000 human PBMC (peripheral blood mononuclear cells) per ml isolated from TB patients in the first phase of infection, or from healthy BCG vaccinated donors, or from healthy contacts to TB patients, the induction being performed by the addition of the polypeptide to a suspension comprising the about 1,000,000 PBMC per ml, the addition of the polypeptide resulting in a concentration of 1-4 μ g polypeptide per ml suspension, the release of IFN- γ being assessable by determination of IFN- γ in supernatant harvested 2 days after the addition of the polypeptide to the suspension; and/or
- 3) induces an IFN- γ release from bovine PBMC derived from animals previously sensitized with mycobacteria belonging to the tuberculosis complex, said release being at least two times the release observed from bovine PBMC derived from animals not previously sensitized with mycobacteria belonging to the tuberculosis complex.

8. A polypeptide fragment according to any of the preceding claims, wherein the sequence identity in c) is at least 80%, such as at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%,
5 at least 97%, at least 98%, at least 99%, and at least 99.5%.

9. A fusion polypeptide comprising at least one polypeptide fragment according to any of the preceding claims and at least one fusion partner.

10. A fusion polypeptide according to claim 56, wherein the
10 fusion partner is selected from the group consisting of a polypeptide fragment as defined in any of claims 1-8, and an other polypeptide fragment derived from a bacterium belonging to the tuberculosis complex, such as ESAT-6 or at least one T-cell epitope thereof, MPB64 or at least one T-cell epitope
15 thereof, MPT64 or at least one T-cell epitope thereof, and MPB59 or at least one T-cell epitope thereof.

11. A fusion polypeptide fragment which comprises

1) a first amino acid sequence including at least one
stretch of amino acids constituting a T-cell epitope
20 derived from the *M. tuberculosis* protein ESAT-6, and a second amino acid sequence including at least one T-cell epitope derived from a *M. tuberculosis* protein different from ESAT-6 and/or including a stretch of amino acids which protects the first amino acid
25 sequence from *in vivo* degradation or post-translational processing; or

2) a first amino acid sequence including at least one
stretch of amino acids constituting a T-cell epitope
derived from the *M. tuberculosis* protein MPT59, and a
30 second amino acid sequence including at least one T-cell epitope derived from a *M. tuberculosis* protein different from MPT59 and/or including a stretch of amino acids which protects the first amino acid

sequence from *in vivo* degradation or post-translational processing.

12. A fusion polypeptide fragment according to claim 11,
wherein the first amino acid sequence is situated C-termi-
5 nally to the second amino acid sequence.
13. A fusion polypeptide fragment according to claim 11,
wherein the first amino acid sequence is situated N-termi-
nally to the second amino acid sequence.
14. A fusion polypeptide fragment according to any of claims
10 11-13, wherein the at least one T-cell epitope included in
the second amino acid sequence is derived from a *M. tubercu-
losis* polypeptide selected from the group consisting of a
polypeptide fragment according to any of claims 1-55, DnaK,
GroEL, urease, glutamine synthetase, the proline rich com-
15 plex, L-alanine dehydrogenase, phosphate binding protein, Ag
85 complex, HBHA (heparin binding hemagglutinin), MPT51,
MPT64, superoxide dismutase, 19 kDa lipoprotein, α -crystal-
lin, GroES, MPT59 when the first T-cell epitope is derived
from ESAT-6, and ESAT-6 when the first T-cell epitope is
20 derived from MPT59.
15. A fusion polypeptide fragment according to any of claims
11-14, wherein the first and second T-cell epitopes each have
a sequence identity of at least 70% with the natively occur-
ring sequence in the proteins from which they are derived.
- 25 16. A fusion polypeptide according to any of claims 11-15,
wherein the first and/or second amino acid sequence have a
sequence identity of at least 70% with the protein from which
they are derived.
17. A fusion polypeptide fragment according to any of claims
30 11-16, wherein the first amino acid sequence is the amino
acid sequence of ESAT-6 or of MPT59 and/or the second amino
acid sequence is the amino acid sequence of a *M. tuberculosis*

polypeptide selected from the group consisting of a polypeptide fragment according to any of claims 1-8, DnaK, GroEL, urease, glutamine synthetase, the proline rich complex, L-alanine dehydrogenase, phosphate binding protein, Ag 85 complex, HBHA (heparin binding hemagglutinin), MPT51, MPT64, superoxide dismutase, 19 kDa lipoprotein, α -crystallin, GroES, ESAT-6 when the first amino acid sequence is that of MPT59, and MPT59 when the first amino acid sequence is that of ESAT-6.

10 18. A fusion polypeptide fragment according to any of claims
11-17, which comprises ESAT-6 fused to MPT59.

19. A fusion polypeptide fragment according to claim 18, wherein no linkers are introduced between the two amino acid sequences.

15 20. A polypeptide according to any of the preceding claims
which is lipidated so as to allow a self-adjuvating effect of
the polypeptide.

21. A substantially pure polypeptide according to any of claims 1-20 for use as a pharmaceutical.

20 22. The use of a substantially pure polypeptide according to any of claims 1-20 in the preparation of a pharmaceutical composition for the diagnosis of or vaccination against tuberculosis caused by *Mycobacterium tuberculosis*, *Mycobacterium africanum* or *Mycobacterium bovis*.

25 23. A nucleic acid fragment in isolated form which

- 1) comprises a nucleic acid sequence which encodes a polypeptide as defined in any of claims 1-20, or comprises a nucleic acid sequence complementary thereto,
- 2) has a length of at least 10 nucleotides and hybridizes readily under stringent hybridization conditions with a

nucleic acid fragment which has a nucleotide sequence selected from

5 SEQ ID NO: 1 or a sequence complementary thereto,
SEQ ID NO: 3 or a sequence complementary thereto,
SEQ ID NO: 5 or a sequence complementary thereto,
SEQ ID NO: 7 or a sequence complementary thereto,
SEQ ID NO: 9 or a sequence complementary thereto,
SEQ ID NO: 11 or a sequence complementary thereto,
SEQ ID NO: 13 or a sequence complementary thereto,
10 SEQ ID NO: 15 or a sequence complementary thereto,
SEQ ID NO: 41 or a sequence complementary thereto,
SEQ ID NO: 47 or a sequence complementary thereto,
SEQ ID NO: 49 or a sequence complementary thereto,
SEQ ID NO: 51 or a sequence complementary thereto,
15 SEQ ID NO: 53 or a sequence complementary thereto,
SEQ ID NO: 55 or a sequence complementary thereto,
SEQ ID NO: 57 or a sequence complementary thereto,
SEQ ID NO: 59 or a sequence complementary thereto,
SEQ ID NO: 61 or a sequence complementary thereto,
20 SEQ ID NO: 63 or a sequence complementary thereto,
SEQ ID NO: 65 or a sequence complementary thereto,
SEQ ID NO: 67 or a sequence complementary thereto,
SEQ ID NO: 69 or a sequence complementary thereto,
SEQ ID NO: 71 or a sequence complementary thereto,
25 SEQ ID NO: 87 or a sequence complementary thereto,
SEQ ID NO: 89 or a sequence complementary thereto,
SEQ ID NO: 91 or a sequence complementary thereto,
SEQ ID NO: 93 or a sequence complementary thereto,
SEQ ID NO: 140 or a sequence complementary thereto,
30 SEQ ID NO: 142 or a sequence complementary thereto,
SEQ ID NO: 144 or a sequence complementary thereto,
SEQ ID NO: 146 or a sequence complementary thereto,
SEQ ID NO: 148 or a sequence complementary thereto,
SEQ ID NO: 150 or a sequence complementary thereto, and
35 SEQ ID NO: 152 or a sequence complementary thereto,

with the proviso that when the nucleic acid fragment comprises a subsequence of SEQ ID NO: 41, then the nucleic acid

fragment contains an A corresponding to position 781 in SEQ ID NO: 41 and when the nucleic acid fragment comprises a subsequence of a nucleotide sequence exactly complementary to SEQ ID NO: 41, then the nucleic acid fragment comprises a T corresponding to position 781 in SEQ ID NO: 41.

24. A nucleic acid fragment according to claim 23, which is a DNA fragment.

25. A vaccine comprising a nucleic acid fragment according to claim 23 or 24, the vaccine effecting in vivo expression of antigen by an animal, including a human being, to whom the vaccine has been administered, the amount of expressed antigen being effective to confer substantially increased resistance to infections with mycobacteria of the tuberculosis complex in an animal, including a human being.

26. A nucleic acid fragment according to claim 23 or 24 for use as a pharmaceutical.

27. The use of a nucleic acid fragment according to claim 23 or 24 in the preparation of a pharmaceutical composition for the diagnosis of or vaccination against tuberculosis caused by *Mycobacterium tuberculosis*, *Mycobacterium africanum* or *Mycobacterium bovis*.

28. An immunologic composition comprising a polypeptide according to any of claims 1-20.

29. An immunologic composition according to claim 28, which further comprises an immunologically and pharmaceutically acceptable carrier, vehicle or adjuvant.

30. An immunologic composition according to claim 29, wherein the carrier is selected from the group consisting of a polymer to which the polypeptide(s) is/are bound by hydrophobic non-covalent interaction, such as a plastic, e.g. polystyrene, a polymer to which the polypeptide(s) is/are covalently

bound, such as a polysaccharide, and a polypeptide, e.g. bovine serum albumin, ovalbumin or keyhole limpet hemocyanin; the vehicle is selected from the group consisting of a diluent and a suspending agent; and the adjuvant is selected from the group consisting of dimethyldioctadecylammonium bromide (DDA), Quil A, poly I:C, Freund's incomplete adjuvant, IFN- γ , IL-2, IL-12, monophosphoryl lipid A (MPL), and muramyl dipeptide (MDP).

31. An immunologic composition according to any of claims 28 to 30, comprising at least two different polypeptide fragments, each different polypeptide fragment being a polypeptide according to any of claims 1-20.

32. An immunologic composition according to claim 31, comprising 3-20 different polypeptide fragments, each different polypeptide fragment being according to any of claims 1-20.

33. An immunologic composition according to any of claims 28-32, which is in the form of a vaccine.

34. An immunologic composition according to any of claims 28-32, which is in the form of a skin test reagent.

35. A vaccine for immunizing an animal, including a human being, against tuberculosis caused by mycobacteria belonging to the tuberculosis complex, comprising as the effective component a non-pathogenic microorganism, wherein at least one copy of a DNA fragment comprising a DNA sequence encoding a polypeptide according to any of claims 1-20 has been incorporated into the genome of the microorganism in a manner allowing the microorganism to express and optionally secrete the polypeptide.

36. A vaccine according to claim 35, wherein the microorganism is a bacterium.

37. A vaccine according to claim 36, wherein the bacterium is selected from the group consisting of the genera *Mycobacterium*, *Salmonella*, *Pseudomonas* and *Eschericia*.
38. A vaccine according to claim 37, wherein the microorganism is *Mycobacterium bovis* BCG, such as *Mycobacterium bovis* BCG strain: Danish 1331.
39. A vaccine according to any of claims 35-38, wherein at least 2 copies of a DNA fragment encoding a polypeptide according to any of claims 1-20 are incorporated into the genome of the microorganism.
40. A vaccine according to claim 39, wherein the number of copies is at least 5.
41. A replicable expression vector which comprises a nucleic acid fragment according to claim 23 or 24.
42. A vector according to claim 41, which is selected from the group consisting of a virus, a bacteriophage, a plasmid, a cosmid, and a microchromosome.
43. A transformed cell harbouring at least one vector according to claim 41 or 42.
44. A transformed cell according to claim 43, which is a bacterium belonging to the tuberculosis complex, such as a *M. tuberculosis bovis* BCG cell.
45. A transformed cell according to claim 43 or 44, which expresses a polypeptide according to any of claims 1-20.
46. A method for producing a polypeptide according to any of claims 1-20, comprising
inserting a nucleic acid fragment according to claim 23 or 24 into a vector which is able to replicate in a host cell,

introducing the resulting recombinant vector into the host cell, culturing the host cell in a culture medium under conditions sufficient to effect expression of the polypeptide, and recovering the polypeptide from the host
5 cell or culture medium; or

isolating the polypeptide from a short-term culture filtrate as defined in claim 1; or

isolating the polypeptide from whole mycobacteria of the tuberculosis complex or from lysates or fractions thereof,
10 e.g. cell wall containing fractions; or

synthesizing the polypeptide by solid or liquid//phase peptide synthesis.

47. A method for producing an immunologic composition according to any of claims 28-32 comprising

15 preparing, synthesizing or isolating a polypeptide according to any of claims 1-20, and

solubilizing or dispersing the polypeptide in a medium for a vaccine, and

20 optionally adding other *M. tuberculosis* antigens and/or a carrier, vehicle and/or adjuvant substance,

or

cultivating a cell according to any of claims 37-45, and

transferring the cells to a medium for a vaccine, and

25 optionally adding a carrier, vehicle and/or adjuvant substance.

48. A method of diagnosing tuberculosis caused by *Mycobacterium tuberculosis*, *Mycobacterium africanum* or *Mycobacterium bovis* in an animal, including a human being, comprising intradermally injecting, in the animal, a polypeptide according to any of claims 1-20 or an immunologic composition according to claim 34, a positive skin response at the location of injection being indicative of the animal having tuberculosis, and a negative skin response at the location of injection being indicative of the animal not having tuberculosis.

49. A method for immunising an animal, including a human being, against tuberculosis caused by mycobacteria belonging to the tuberculosis complex, comprising administering to the animal the polypeptide according to any of claims 1-20, the immunologic composition according to claim 33, or the vaccine according to any of claims 35-40.

50. A method according to claim 49, wherein the polypeptide, immunologic composition, or vaccine is administered by the parenteral (such as intravenous and intraarterially), intraperitoneal, intramuscular, subcutaneous, intradermal, oral, buccal, sublingual, nasal, rectal or transdermal route.

51. A method for diagnosing ongoing or previous sensitization in an animal or a human being with bacteria belonging to the tuberculosis complex, the method comprising providing a blood sample from the animal or human being, and contacting the sample from the animal with the polypeptide according to any of claims 1-20, a significant release into the extracellular phase of at least one cytokine by mononuclear cells in the blood sample being indicative of the animal being sensitized.

52. A composition for diagnosing tuberculosis in an animal, including a human being, comprising a polypeptide according to any of claims 1-20, or a nucleic acid fragment according to claim 23 or 24, optionally in combination with a means for detection.

53. A monoclonal or polyclonal antibody, which is specifically reacting with a polypeptide according to any of claims 1-20 in an immuno assay, or a specific binding fragment of said antibody.

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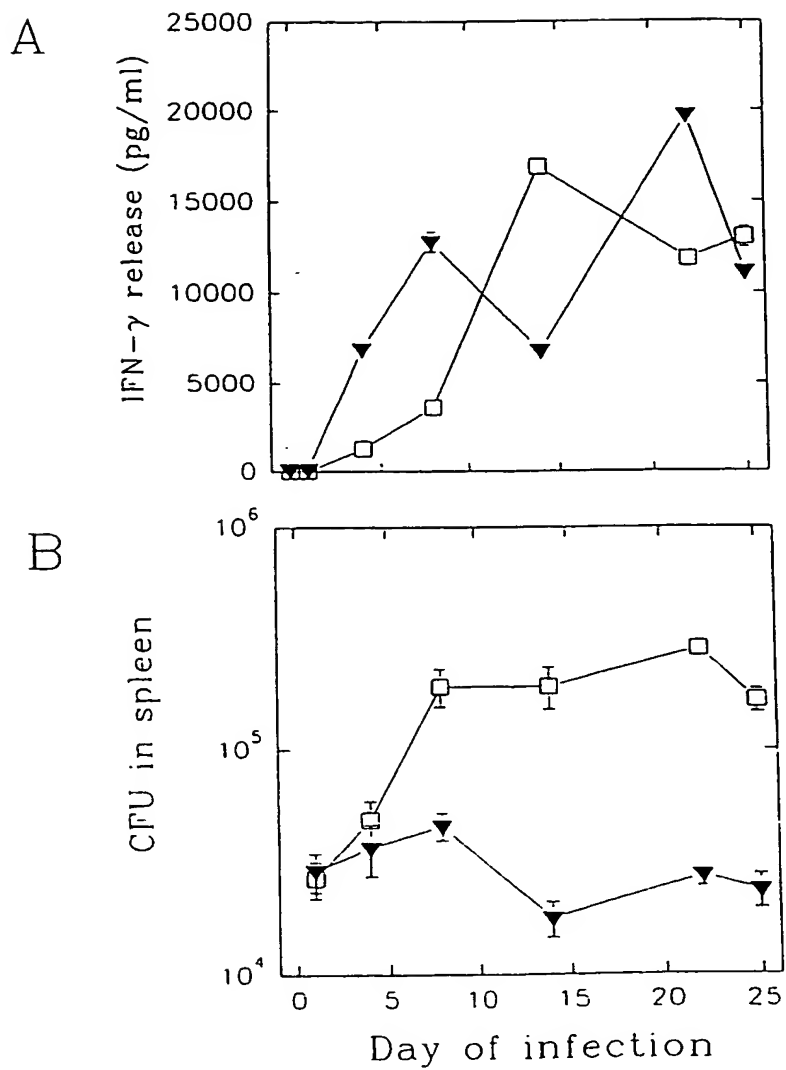
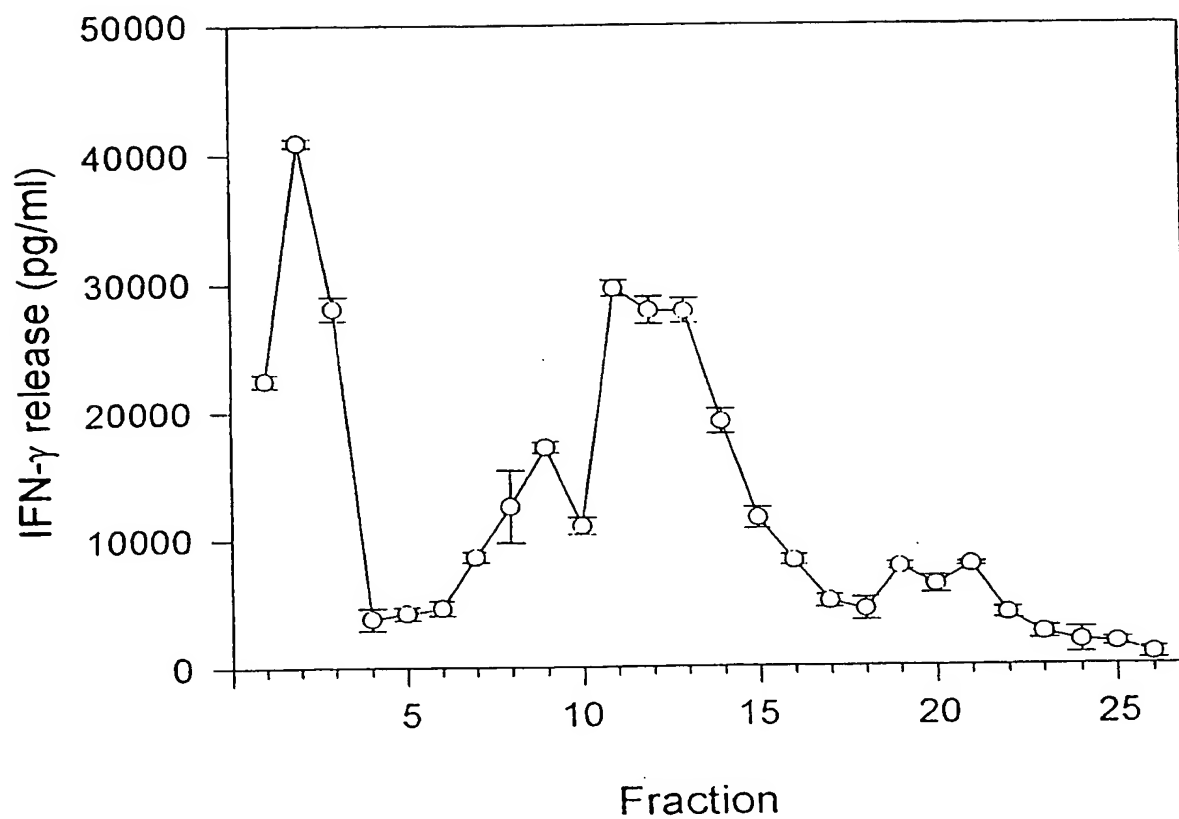


Fig. 1

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**Fig. 2**

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1	GGCCGCCCGGT	ACCTATGTTGG	CCGCCGATGC	TGCGGNCGCG	TCGACCTATA	CCGGTTCTG	60
		-35 region			-10 region		
51	ATCGAACCCCT	GCTGACCGAG	AGGACTTGTG	ATG TCG CAA	ATC ATG TAC AAC	TAC CCC GCG	120
		Shine Delgarno	M S Q	I M Y	N Y P	A	
121	ATG TTG GGT	CAC GCC GGG	GAT ATG GCC	GGA TAT GCC	GGC ACG CTG	CAG AGC TTG GGT GCC	180
	M L G	H A G	D M A	G Y A	G T L	Q S L G A	
181	GAG ATC GCC	GTG GAG CAG	GCC GCC	GCG TTG	CAG AGT GCG	TGG CAG GGC GAT ACC GGG ATC ACG	240
	E I A	V E Q	A A L	A Q S	A W Q	G D T G I T	
241	TAT CAG GCG	TGG CAG GCA	CAG TGG	AAC CAG	GCC ATG GAA	GAT TTG GTG CCG GCC TAT CAT	300
	Y Q A	W Q A	Q W N	Q A M	E D L	V R Y H A	
301	GCG ATG TCC	AGC ACC CAT	GAA GCC	AAC ACC	ATG GCG	ATG ATG GCC CGC GAC ACC GCC GAA	360
	Y M S	S S T	H E A	N T M	A M M	- A R D T A E	
361	GCC GCC AAA	TGG GGC GGC	TAG				381
	A A K	W G G	*				

Fig. 3

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1 GGGTAGCCCG ACCACGGCTG GGCAAAGATG TGCAGGCCGC CATCAAGGCG GTCAAGGCCG 60
 -35 region
 61 GCGACGGCGT CATAAACCCG GACGGCACCT TGTGCGGG CCCC GCGTG CTGACGCCCG 120
 -10 region
 121 ACGAGTACAA CTCCCGGCTG GTG GCC GAC CCG GAG TCC ACC GCG GCG 170
 Shine Delgarno V A A D P E S T A A
 171 TTG CCC GAC GGC GCC GGG CTG GTC GTT CTG GAT GGC ACC GTC ACT GCC GAA CTC GAA GCC 230
 L P D G A G L V V L D G T V T A E L E A
 231 GAG GGC TGG GCC AAA GAT CGC ATC CGC GAA CTG CAA GAG CTG CGT AAG TCG ACC GGG CTG 290
 E G W A K D R I R E L Q E L R K S T G L
 291 GAC GTT TCC GAC CGC ATC CGG GTG GTG ATG TCG GTG CCT GCG GAA CGC GAA GAC TGG GCG 350
 D V S D R I R V V M S V P A E R E D W A
 351 CGC ACC CAT CGC GAC CTC ATT GCC GGA GAA ATC TTG GCT ACC GAC TTC GAA TTC GCC GAC 410
 R T H R D L I A G E I L A T D F E F A D
 411 CTC GCC GAT GGT GTG GCC ATC GGC GAC GGC GTG CGG GTA AGC ATC GAA AAG ACC TGA 467
 L A D G V A I G D G V R V S I E K T *

1	GAA7TCGCCGGGTGCACACAGCCTTACACGACGGA <u>AGGT</u> TGGACATGAAG	50
		M K
51	GGTCGGTTCGGCGCTGCTGCGGGCGCTCTGGATTGCCGCACTGTCATTTCGG	100
	G R S A L L R A L W I A A L S F G	
101	GTTGGGCGGTGTCTCGCGGTAGCCGCGGAACCCACCGCCAAGGCCGCCCAT	150
	L G G V A V A A E P T A K A A P	
151	ACGAGAACCTGATGGTGCCGTCGCCCTCGATGGGCCGGGACATCCCGGTG	200
	Y E N L M V P S P S M G R D I P V	
201	GCCTTCCTAGCCGGTGGGCGCGCACGCGGTGTATCTGCTGGACGCCTTCAA	250
	A F L A G G P H A V Y L L D A F N	
251	CGCCGGCCCGGATGTCAGTAACTGGGTCAACGCGGGTAACGCGATGAACA	300
	A G P D V S N W V T A G N A M N	
301	CGTTGGCGGGCAAGGGGATTTCGGTGGTGGCACCGGCCGGTGGTGCGTAC	350
	T L A G K G I S V V A P A G G A Y	
351	AGCATGTACACCAACTGGGAGCAGGATGGCAGCAAGCAGTGGGACACCTT	400
	S M Y T N W E Q D G S K Q W D T F	
401	CTTGTCCGCTGAGCTGCCCCACTGGCTGGCCGCTAACCGGGGCTTGGCCC	450
	L S A E L P D W L A A N R G L A	
451	CCGGTGGCCATGCGGCCGTTGGCGCCGCTCAGGGCGGTTACGGGGCGATG	500
	P G G H A A V G A A Q G G Y G A M	
501	GCGCTGGCGGCCTTCCACCCCGACCGCTTCGGCTTCGCTGGCTCGATGTC	550
	A L A A F H P D R F G F A G S M S	
551	GGGCTTTTGTACCCGTCGAACACCACCACCAACGGTGCGATCGCGGCGG	600
	G F L Y P S N T T T N G A I A A	
601	GCATGCAGCAATTCGGCGGTGTGGACACCAACCGAATGTGGGGAGCACCA	650
	G M Q Q F G G V D T N G M W G A P	
651	CAGCTGGGTTCGGTGGAAAGTGGCACGACCCGTGGGTGCATGCCAGCCTGCT	700
	Q L G R W K W H D P W V H A S L L	
701	GGCGCAAAACAACACCCGGGTGTGGGTGTGGAGCCCGACCAACCCGGGAG	750
	A Q N N T R V W V W S P T N P G	
751	CCAGCGATCCCGCCGCCATGATCGGCCAA <u>ACCG</u> CCGAGGCGATGGGTAAC	800
	A S D P A A M I G Q T A E A M G N	
801	AGCCGCATGTTCTACAACCAAGTATCGCAGCGTCGGCGGGCACAACGGACA	850
	S R M F Y N Q Y R S V G G H N G H	
851	CTTCGACTTCCCAGCCAGCGGTGACAACGGCTGGGGCTCGTGGGCGCCCC	900
	F D F P A S G D N G W G S W A P	
901	AGCTGGGCGCTATGTCTGGGCGATATCGTCGGTGGCATCCGCTAAGCGAAT	950
	Q L G A M S G D I V G A I R .	
951	TC	952

SUBSTITUTE SHEET (RULE 26)

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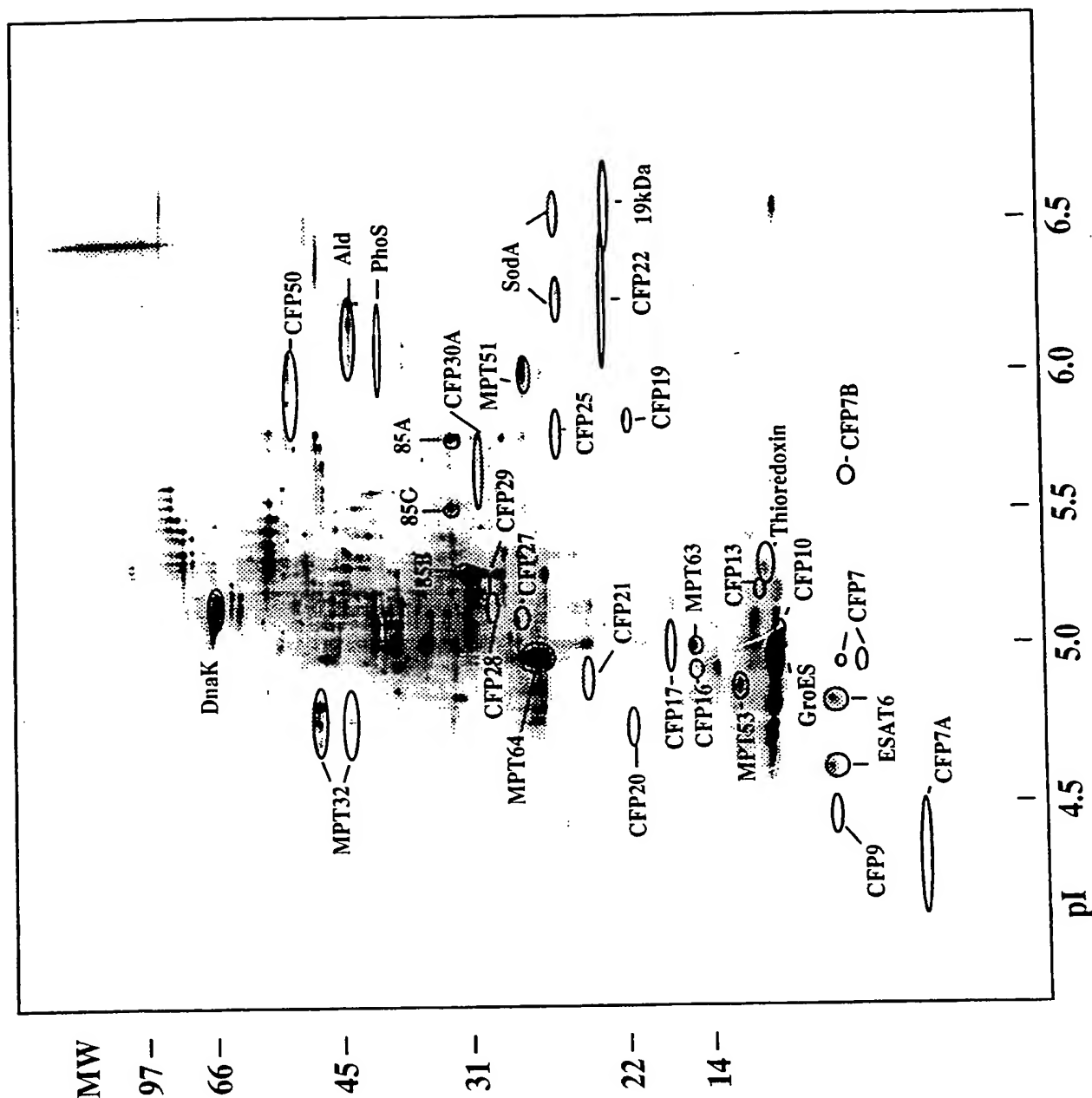


Fig. 6

SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International Application No

PCT/DK 98/00132

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 A61K39/04 C07K14/35 C12N15/62 A61K38/16
G01N33/569 C12Q1/68 C07K16/12

According to International Patent Classification(IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A61K C07K G01N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 97 09428 A (CORIXA CORP) 13 March 1997</p> <p>see the claims see abstract; examples 1,3 see page 12 - page 18 see page 21 - page 25 ---</p> <p style="text-align: center;">-/--</p>	<p>1-4,6,7, 9-13,15, 16, 21-43, 45-53</p>

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

1 September 1998

Date of mailing of the international search report

15. 09. 1998

Name and mailing address of the ISA

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Authorized officer

Oderwald, H

INTERNATIONAL SEARCH REPORT

In. .ational Application No

PCT/DK 98/00132

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>WO 97 09429 A (CORIXA CORP) 13 March 1997</p> <p>see the claims see abstract; examples 1,3 see page 12 - page 15, paragraph 2 see page 17, paragraph 4 - page 19, paragraph 2 see page 24 - page 25</p>	<p>1-4,6,7, 9-13,15, 16, 21-43, 45-47, 49-53</p>
X	<p>WO 95 01441 A (STATENS SERUMSINSTITUT ;ANDERSEN PETER (DK); ANDERSEN AASE BENGAAR) 12 January 1995</p> <p>see the claims see abstract; figure 10; examples 1,3-6; table 2 see page 12 - page 32 see page 12, paragraph 3</p>	<p>1-4,6,7, 20-53</p>
X	<p>SORENSEN A L ET AL: "Purification and characterization of a low-molecular-mass T-cell antigen secreted by Mycobacterium tuberculosis." INFECTION AND IMMUNITY, (1995 MAY) 63 (5) 1710-7. JOURNAL CODE: G07. ISSN: 0019-9567., XP002068818 cited in the application see abstract; figures 4-6 see page 1710, paragraph 3 - page 1712, paragraph 4 see page 1713, paragraph 5. see page 1716, paragraph 5 - paragraph 8</p>	<p>1-4,6,7, 9,10, 21-24, 28,33, 34, 41-43, 45-53</p>
X	<p>CRABTREE J AND ROE B A: "Homo sapiens clone 137c7" EMBL SEQUENCE DATABASE, 19 March 1997, XP002068854 HEIDELBERG, GERMANY see the whole document</p>	<p>23-27, 41-43</p>
X	<p>VALDES-STAUER N AND SCHERER S: "Nucleotide sequence and taxonomical distribution of the bacteriocin gene lin cloned from Brevibacterium linens M18" APPLIED AND ENVIRONMENTAL MICROBIOLOGY, vol. 62, no. 4, April 1996, pages 1283-1286, XP002076056 see the whole document</p>	<p>1-4,6,8, 23,24, 41-43, 45,46,52</p>

-/--

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 37219 A (UNIV CALIFORNIA ;HORWITZ MARCUS A (US); HARTH GUENTER (US)) 28 November 1996 see the claims see abstract; figures 2-4,13; examples 4,6,14,21-26 -----	
P,X	BROWN D AND CHURCHER C M: "Mycobacterium tuberculosis cosmid v035" EMBL SEQUENCE DATABASE, 20 February 1998, XP002068855 HEIDELBERG, GERMANY see the whole document -----	23-27, 41-43
T	ROSENKRANDS I ET AL: "Identification and characterization of a 29-kilodalton protein from Mycobacterium tuberculosis culture filtrate recognized by mouse memory effector cells" INFECTION AND IMMUNITY, vol. 66, no. 6, June 1998, pages 2718-2735, XP002076057 see abstract; figure 4 see page 2728, paragraph 4 - page 2729, paragraph 20 -----	1-4,6-9, 23,24, 41-46, 52,53
P,X	& ROSENKRANDS I ET AL: "CFP29 protein (accession number 007812)" EMBL SEQUENCE DATABASE, 1 July 1997, Heidelberg, Germany see the whole document -----	1-4,6-8
P,X	& ROSENKRANDS I ET AL: "Mycobacterium tuberculosis cfp29 gene (accession number Y12820)" EMBL SEQUENCE DATABASE, 30 June 1997, Heidelberg, Germany see the whole document -----	23,24, 41-46,52

INTERNATIONAL SEARCH REPORT

International application No.
PCT/DK 98/00132

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Although claims 49 and 50 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-4,6-17,20-53; inventions 1 and 8
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-4, 6-17, 20-53 all partially

A polypeptide fragment from mycobacteria belonging to the tuberculosis complex comprising the amino acid SEQ ID NO: 2, nucleic acids encoding said polypeptide as in SEQ ID NO:1, fusion proteins comprising said polypeptides, vaccines, pharmaceutical and immunological compositions containing said polypeptide or nucleic acid, an expression vector comprising said nucleic acid, a host transformed with said vector, immunization with said polypeptide, the use of said polypeptide in diagnosis, antibodies against said polypeptide.

2. Claims: 1-4, 6-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 4 and 3.

3. Claims: 1-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 6, 5 and 17.

4. Claims: 1-4, 6-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 8, 7 and 18.

5. Claims: 1-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 10, 9 and 19.

6. Claims: 1-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 12, 11 and 20.

7. Claims: 1-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 14, 13 and 21.

8. Claims: 1-4, 6-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 16, 15 and 23.

9. Claims: 1-4, 6-17, 20-53 all partially

same as invention 1 but for SEQ ID NO: 22.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

10. Claims: 1-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 42 and 41.
11. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 48, 47 and 81.
12. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 50, 49 and 82.
13. Claims: 1-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 52 and 51.
14. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 54, 53 and 83.
15. Claims: 1-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 56 and 55.
16. Claims: 1-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 58, 57 and 84.
17. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 60, 59 and 85.
18. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 62, 61 and 86.
19. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 64, 63 and 79.
20. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 66, 65 and 78.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

21. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 68 and 67.
22. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 70 and 69.
23. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 72 and 71.
24. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 75.
25. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 76.
26. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 80.
27. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 88 and 87.
28. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 90 and 89.
29. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 92 and 91.
30. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 94 and 93.
31. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 141, 140 and 169.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

32. Claims: 1-4, 6-17, 20-53 all partially
same in invention 1 but for SEQ ID NO: 143, 142 and 170.

33. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 145, 144 and 171.

34. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 147, 146 and 168.

35. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 149, 148 and 73.

36. Claims: 1-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 151, 150 and 74.

37. Claims: 1-4, 6-17, 20-53 all partially
same as invention 1 but for SEQ ID NO: 153, 152 and 77.

38. Claims: 11-17, 20-53 all partially, 18, 19

A fusion polypeptide comprising ESAT-6 or MPT59 each individually with one of the following epitope partners: DnaK, GroEL, urease, glutamine synthetase, the proline rich complex, L-alanine dehydrogenase, phosphate binding protein, Ag 85 complex, HBHA, MPT51, MPT64, superoxide dismutase 19 kDa lipoprotein, alpha-crystallin, GroES, nucleic acids encoding said polypeptide, vaccines, pharmaceutical and immunological compositions containing said polypeptide or nucleic acid, an expression vector comprising said nucleic acid, a host transformed with said vector, immunization with said polypeptide, the use of said polypeptide in diagnosis, antibodies against said polypeptide.

INTERNATIONAL SEARCH REPORT

Information on patent family members

In. ational Application No

PCT/DK 98/00132

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9709428 A	13-03-1997	AU 7158696 A EP 0851927 A NO 980883 A	27-03-1997 08-07-1998 27-04-1998
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WO 9637219 A	28-11-1996	AU 6024596 A EP 0828510 A	11-12-1996 18-03-1998